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 Candia III, Albert F.
 Arbbor Vita Corporation

<120> CLASP-2 TRANSMEMBRANE PROTEINS

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 Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
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 Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
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 Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
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 Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
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 Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
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Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg	
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Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp	
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Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr	
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Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser	
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 Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
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Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser	
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His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala	
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Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser	
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His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp	
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His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val	
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 aag gag ctt tct gaa atc atg cat gag cag atc tgc ccc ctg gag gag 3600
 Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu
 1185 1190 1195 1200

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 Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
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 145 150 155 160

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Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
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 Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys
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His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Ala	Tyr	Ser	Lys	Val	Thr	Glu	Val	
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Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu
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Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
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Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
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Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
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Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
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Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly

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Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser			
145	150	155	160
ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc cag			529
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln			
165	170	175	
gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa agg			577
Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg			
180	185	190	
aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt gag			625
Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu			
195	200	205	
atg cca ttt acg cag acc ggg aag agg cag ggc ggc gtg gaa gag cag			673
Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln			
210	215	220	
tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat gtg			721
Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val			
225	230	235	240
aag aag cgc atc cct ttc atg tac cag cac cac act gac ctg aac ccc			769
Lys Lys Arg Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro			
245	250	255	
atc gag gtc cat tga cgagatgagt aagaaggtgg cggagctccg gcagctgtgc			824
Ile Glu Val His			
260			
tcctcggccg aggtggacat gatcaaactg cagctcaaac tccagggcag cgtgagtgtt			884
caggtcaatg ctggcccact agcatatgcg cgagctttct tagatgatac aaacacaaag			944
cgatatcctg acaataaagt gaagctgctt aaggaagttt tcaggcaatt tgtggaagct			1004
tgcggtcaag ccttagcggt aaacgaacgt ctgattaaag aagaccagct cgagtatcag			1064
gaagaaatga aagccaacta cagggaaatg gcgaaggagc tttctgaaat catgcatgag			1124
cagatctgcc ccctggagga gaagacgagc gtcttaccga attcccttca catcttcaac			1184
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gtgtga			1250

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 (CLASP-2C)

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 Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
 35 40 45
 Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
 50 55 60
 Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
 65 70 75 80
 Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
 85 90 95
 Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly
 100 105 110
 Gln Gly Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu
 115 120 125
 Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 130 135 140
 Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
 145 150 155 160
 Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
 165 170 175
 Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg
 180 185 190
 Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu
 195 200 205
 Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln
 210 215 220
 Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val
 225 230 235 240
 Lys Lys Arg Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro
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 Ile Glu Val His
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 (CLASP-2D) KIAA1058

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 Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
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caa gac agc aat aag cta tcc aat gat gac atg ctc aag tta ctt gca	96
Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala	
20 25 30	
gac ttt cgg aaa cct gag aag atg gct aag ctc cca gtg att tta ggc	144
Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly	
35 40 45	
aat cta gac att aca att gat aat gtt tcc tca gac ttc cct aat tat	192
Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr	
50 55 60	
gtt aat tca tca tac att ccc aca aaa caa ttt gaa acc tgc agt aaa	240
Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys	
65 70 75 80	
act ccc atc acg ttt gaa gtg gag gaa ttt gtg ccc tgc ata cca aaa	288
Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys	
85 90 95	
cac act cag cct tac acc atc tac acc aat cac ctt tac gtt tat cct	336
His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro	
100 105 110	
aag tac ttg aaa tac gac agt cag aag tct ttt gcc aag gct aga aat	384
Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn	
115 120 125	
att gcg att tgc att gaa ttc aaa gat tca gat gag gaa gac tct cag	432
Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln	
130 135 140	
ccc ctt aag tgc att tat ggc aga cct ggt ggg cca gtt ttc aca aga	480
Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg	
145 150 155 160	
agc gcc ttt gct gca gtt tta cac cat cac caa aac cca gaa ttt tat	528
Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr	
165 170 175	
gat gag att aaa ata gag ttg ccc act cag ctg cat gaa aag cac cac	576
Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His	
180 185 190	
ctg ttg ctc aca ttc ttc cat gtc agc tgt gac aac tca agt aaa gga	624
Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly	
195 200 205	
agc acg aag aag agg gat gtc gtt gaa acc caa gtt ggc tac tcc tgg	672
Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp	
210 215 220	
ctt ccc ctc ctg aaa gac gga agg gtg gtg aca agc gag cag cac atc	720
Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile	
225 230 235 240	
ccg gtc tcg gcg aac ctt cct tcg ggc tat ctt ggc tac cag gag ctt	768
Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu	
245 250 255	
ggg atg ggc agg cat tat ggt ccg gaa att aaa tgg gta gat gga ggc	816

Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly		
			260					265					270				
aag	cca	ctg	ctg	aaa	att	tcc	act	cat	ctg	gtt	tct	aca	gtg	tat	act	864	
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr		
		275					280					285					
cag	gat	cag	cat	tta	cat	aat	ttt	ttc	cag	tac	tgt	cag	aaa	acc	gaa	912	
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu		
	290					295					300						
tct	gga	gcc	caa	gcc	tta	gga	aac	gaa	ctt	gta	aag	tac	ctt	aag	agt	960	
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser		
305					310					315					320		
ctg	cat	gcg	atg	gaa	ggc	cac	gtg	atg	atc	gcc	ttc	ttg	ccc	act	atc	1008	
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile		
				325					330					335			
cta	aac	cag	ctg	ttc	cga	gtc	ctc	acc	aga	gcc	aca	cag	gaa	gaa	gtc	1056	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val		
			340					345					350				
gcg	gtt	aac	gtg	act	cgg	gtc	att	att	cat	gtg	gtt	gcc	cag	tgc	cat	1104	
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His		
		355					360					365					
gag	gaa	gga	ttg	gag	agc	cac	ttg	agg	tca	tat	gtt	aag	tac	gcg	tat	1152	
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr		
	370					375					380						
aag	gct	gag	cca	tat	gtt	gcc	tct	gaa	tac	aag	aca	gtg	cat	gaa	gaa	1200	
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu		
385					390					395					400		
ctg	acc	aaa	tcc	atg	acc	acg	att	ctc	aag	cct	tct	gcc	gat	ttc	ctc	1248	
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu		
			405						410					415			
acc	agc	aac	aaa	cta	ctg	aag	tac	tca	tgg	ttt	ttc	ttt	gat	gta	ctg	1296	
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu		
			420					425					430				
atc	aaa	tct	atg	gct	cag	cat	ttg	ata	gag	aac	tcc	aaa	gtt	aag	ttg	1344	
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu		
		435					440					445					
ctg	cga	aac	cag	aga	ttt	cct	gca	tcc	tat	cat	cat	gca	gtg	gaa	acc	1392	
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr		
	450					455					460						
gtt	gta	aat	atg	ctg	atg	cca	cac	atc	act	cag	aag	ttt	cga	gat	aat	1440	
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn		
465					470					475					480		
cca	gag	gca	tct	aag	aac	gcg	aat	cat	agc	ctt	gct	gtc	ttc	atc	aag	1488	
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys		
				485					490					495			
aga	tgt	ttc	acc	ttc	atg	gac	agg	ggc	ttt	gtc	ttc	aag	cag	atc	aac	1536	
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn		

500					505					510					
aac tac att agc tgt ttt gct cct gga gac cca aag acc ctc ttt gaa	1584														
Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu															
515	520														
tac aag ttt gaa ttt ctc cgt gta gtg tgc aac cat gaa cat tat att	1632														
Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile															
530	535														
ccg ttg aac tta cca atg cca ttt gga aaa ggc agg att caa aga tac	1680														
Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr															
545	550														
caa gac ctc cag ctt gac tac tca tta aca gat gag ttc tgc aga aac	1728														
Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn															
565	570														
cac ttc ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag	1776														
His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln															
580	585														
gag ttc cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg	1824														
Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu															
595	600														
ctg ata aag cat tct ttt gat gac aga tat gct tca agg agc cat cag	1872														
Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln															
610	615														
gca agg ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa	1920														
Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu															
625	630														
aac gtc cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac	1968														
Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn															
645	650														
gcg ggc atg act gtg aag gat gaa tcc ctg gct cta cca gct gtg aat	2016														
Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn															
660	665														
ccg ctg gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac	2064														
Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His															
675	680														
aag gac ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc	2112														
Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr															
690	695														
tca act cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct	2160														
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser															
705	710														
ctc ata agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag	2208														
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu															
725	730														
aag agc aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat	2256														
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn															
740	745														
	750														

tcc gtg gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta	2304
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu	
755 760 765	
ctg atg tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg	2352
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu	
770 775 780	
ttt aca tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt	2400
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe	
785 790 795 800	
aca ata tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga	2448
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg	
805 810 815	
tac ata gcc aga aca gga atg atg cat gcc aga ttg cag cag ctg ggc	2496
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly	
820 825 830	
agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac tcg gac	2544
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp	
835 840 845	
gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct act gag	2592
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu	
850 855 860	
gtt tgc ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg ttt	2640
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe	
865 870 875 880	
aag aac cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa aaa	2688
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys	
885 890 895	
gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct gaa acg	2736
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr	
900 905 910	
gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat aag ttt	2784
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe	
915 920 925	
ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct ctg tgt	2832
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys	
930 935 940	
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Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr	
945 950 955 960	
gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt gat tac	2928
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr	
965 970 975	
act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc ata tct	2976
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser	
980 985 990	

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Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe	
995 1000 1005	
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Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu	
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Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg	
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ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat gag aac	3168
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn	
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gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa tcc tat	3216
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr	
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gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg gcc agg	3264
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg	
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atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc tat gtc	3312
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val	
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cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa gaa gca gtc	3360
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val	
1105 1110 1115 1120	
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Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg	
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agg agc cgg gga ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc	3456
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val	
1140 1145 1150	
att acc cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg	3504
Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly	
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Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu	
1170 1175 1180	
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Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala	
1185 1190 1195 1200	
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Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys	
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gtg acc gag gtc atg cac tcg ggc cgc agg ctt ctg ggg acc tac ttc	3744

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe	
1235 1240 1245	
cgg gta gcc ttc ttc ggg cag gca gcg caa tac cag ttt aca gac agt	3792
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser	
1250 1255 1260	
gaa aca gat gtg gag gga ttc ttt gaa gat gaa gat gga aag gag tat	3840
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Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg	
1285 1290 1295	
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Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met	
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ata cag gat tct ggc aag gtc aac cct aag gat ctg gat tct aag tat	3984
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr	
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gcc tac atc cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag	4032
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu	
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Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly	
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Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys	
1380 1385 1390	
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Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr	
1395 1400 1405	
gac ctg aac ccc atc gag gtg gcc att gac gag atg agt aag aag gtg	4272
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val	
1410 1415 1420	
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Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys	
1425 1430 1435 1440	
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Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly	
1445 1450 1455	
cca cta gca tat gcg cga gct ttc tta gat gat aca aac aca aag cga	4416
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg	
1460 1465 1470	
tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt ttc agg caa ttt	4464
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe	

1475	1480	1485	
gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa cgt ctg att aaa			4512
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys			
1490	1495	1500	
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Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
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Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
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Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
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Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
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His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
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Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
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Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
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Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
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Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
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Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
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Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
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Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
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Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
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Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
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Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
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Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
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Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
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 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
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 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
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 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
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 450 455 460
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
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 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
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 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
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 Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
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 Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
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 Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
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 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
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 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
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 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
 610 615 620
 Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu

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Asn Val Gln Arg	Ile Asn Val Arg Asp	Val Ser Pro Phe Pro Val Asn				
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Ala Gly Met Thr	Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn					
	660	665			670	
Pro Leu Val Thr	Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His					
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Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr						
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Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser						
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Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu						
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Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn						
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Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu						
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Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu						
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Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe						
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Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg						
	805	810				815
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly						
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Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp						
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Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu						
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Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe						
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Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys						
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Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr						
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Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe						
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Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys						
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Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr						
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 Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
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2E)

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Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val
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Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
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Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
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Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
          65           70           75           80

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Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
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Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
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Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln	
1140 1145 1150	
gaa gaa atg aaa gcc aac tac agg gaa atg gcg aag gag ctt tct gaa	3504
Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu	
1155 1160 1165	
atc atg cat gag cag atc tgc ccc ctg gag gag aag acg agc gtc tta	3552
Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu	
1170 1175 1180	
ccg aat tcc ctt cac atc ttc aac gcc atc agt ggg act cca aca agc	3600
Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser	
1185 1190 1195 1200	
aca atg gtt cac ggg atg acc agc tcg tct tcg gtc gtg tga	3642
Thr Met Val His Gly Met Thr Ser Ser Ser Ser Val Val	

1205

1210

<210> 10
 <211> 1213
 <212> PRT
 <213> Homo sapiens
 <223> Human cadherin-like asymmetry protein 2E (CLASP
 2E)

<400> 10

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Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	Val
			20					25					30		
Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu
		35					40					45			
Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala
	50					55				60					
Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr
	65				70				75					80	
Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	Ser
				85				90						95	
Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	Lys
			100					105					110		
Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg
		115					120					125			
Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val
	130					135					140				
Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu
	145				150					155				160	
Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys
			165					170						175	
Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr
			180				185						190		
Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys
		195				200						205			
Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu
	210				215					220					
Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp
	225				230				235					240	
Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe
			245					250						255	
Leu	Val	Gly	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	
		260				265						270			
Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile
		275				280						285			
Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg
	290				295					300					
Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val
	305				310				315					320	
Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly
			325					330					335		
Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu
		340					345					350			
Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp
	355					360					365				
Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr
	370				375					380					
Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile
	385				390				395					400	

Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser		
				405					410					415			
Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val		
			420					425					430				
Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met		
		435					440					445					
Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr		
	450					455					460						
Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile		
465					470					475					480		
Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	Tyr	Ile		
			485					490						495			
Ala	Arg	Asn	Gln	Glu	Gly	Leu	Gly	Pro	Ile	Val	His	Asp	Arg	Lys	Ser		
		500						505					510				
Gln	Thr	Leu	Pro	Val	Ser	Arg	Asn	Arg	Thr	Gly	Met	Met	His	Ala	Arg		
		515					520					525					
Leu	Gln	Gln	Leu	Gly	Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser		
		530				535					540						
Tyr	Gly	His	Ser	Asp	Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala		
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Asn	Ile	Ala	Thr	Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu		
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Phe	Thr	Leu	Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn		
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Pro	Leu	Met	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys		
		595				600						605					
His	Gln	Ser	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser		
	610				615						620						
Leu	Ile	Tyr	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met		
625				630						635					640		
Cys	Ala	Ala	Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu		
			645					650						655			
Ser	Ser	Ile	Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg		
		660						665					670				
Asn	Asn	Phe	Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu		
		675				680						685					
Gln	Val	Ile	Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile		
	690					695					700						
Gly	Glu	Thr	Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala		
705				710						715					720		
Asn	Ser	Asp	Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys		
			725					730						735			
Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met		
		740						745					750				
Lys	Glu	His	Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser		
		755				760						765					
Leu	Ala	Lys	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu		
	770					775					780						
Asp	Ser	Met	Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala		
785				790						795					800		
Ala	Met	Cys	Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr		
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Arg	Lys	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr		
		820						825						830			
Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Lys	Ala		
		835				840						845					
Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys	Leu	Ile	Ile	Pro	Ile		
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Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Glu	Arg	Leu	Ala	His	Leu	Tyr	Asp	Thr		
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<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by insertion of 69 nucleotides at position
2927 of human CLASP-2A found in human CLASP-2D.

<400> 12

Ala Val Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys
1 5 10 15

Leu Arg Arg Ser Arg Gly
20

<210> 13

<211> 165

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Insertion at
position 3153, entire sequence insertion in human
CLASP-2D, portion of insertion in human CLASP-2B,
2C and 2E

<400> 13

tgagaggctg gccatctgt atgacacgct gcaccgggcc tacagcaaag tgaccgaggt 60
catgcactcg ggccgcaggc ttctggggac ctacttccgg gtagccttct tcgggcaggc 120
agcgcaatac cagtttacag acagtgaaac agatgtggag ggatt 165

<210> 14

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acids
encoded by entire insertion at position 3153 of
human CLASP-2A found in human CLASP-2D

<400> 14

Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
1 5 10 15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
20 25 30

Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
35 40 45

Glu Thr Asp Val Glu Gly
50

<210> 15

<211> 40

<212> PRT

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Amino acids
        encoded by insertion at position 3153 of human
        CLASP-2A found in human CLASP-2B, 2C and 2E

<400> 15
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1             5             10             15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
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Arg Val Ala Phe Phe Gly Gln Gly
      35             40

<210> 16
<211> 3614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)..(2864)

<220>
<223> Human cadherin-like asymmetry protein 2A-80
        (CLASP-2A-80)

<400> 16
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  Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
    1             5             10             15

ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc      95
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
          20             25             30

cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata      143
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
          35             40             45

aag cat tct ttt gat gac aga tat gct tca agg agc cat cag gca agg      191
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
          50             55             60

ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc      239
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
        65             70             75

cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc      287
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
        80             85             90             95

atg acc gtg aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg      335
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
          100             105             110

gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac aag gac      383
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp

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115	120	125	
ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc tca act Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr 130 135 140			431
cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct ctc ata Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile 145 150 155			479
agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser 160 165 170 175			527
aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat tcc gtg Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val 180 185 190			575
gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta ctg atg Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met 195 200 205			623
tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg ttt aca Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr 210 215 220			671
tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile 225 230 235			719
tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile 240 245 250 255			767
gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser 260 265 270			815
cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg 275 280 285			863
ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser 290 295 300			911
tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala 305 310 315			959
aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu 320 325 330 335			1007
ttt aca ttg gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn 340 345 350			1055
cct ctc atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys 355 360 365			1103

cat cag tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc	1151
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser	
370 375 380	
tta att tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg	1199
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met	
385 390 395	
tgt gcg gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg	1247
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu	
400 405 410 415	
agc tcc atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg	1295
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg	
420 425 430	
aac aac ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg	1343
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu	
435 440 445	
caa gtc atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att	1391
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile	
450 455 460	
ggg gaa acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc	1439
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala	
465 470 475	
aac agt gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag	1487
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys	
480 485 490 495	
gac tta acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg	1535
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met	
500 505 510	
aag gag cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc	1583
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser	
515 520 525	
ctg gcc aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc	1631
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu	
530 535 540	
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Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala	
545 550 555	
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Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr	
560 565 570 575	
cgg aaa ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc	1775
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr	
580 585 590	
cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag	1823
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln	
595 600 605	

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tac aaa ctt atc atc ccc att tat gag aag cgg agg gat ttc ttt gaa Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu 640 645 650 655	1967
gat gaa gat gga aag gag tat att tac aag gaa ccc aaa ctc aca ccg Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro 660 665 670	2015
ctg tcg gaa att tct cag aga ctc ctt aaa ctg tac tcg gat aaa ttt Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe 675 680 685	2063
ggt tct gaa aat gtc aaa atg ata cag gat tct ggc aag gtc aac cct Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro 690 695 700	2111
aag gat ctg gat tct aag tat gca tac atc cag gtg act cac gtc atc Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile 705 710 715	2159
ccc ttc ttt gac gaa aaa gag ttg caa gaa agg aaa aca gag ttt gag Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu 720 725 730 735	2207
aga tcc cac aac atc cgc cgc ttc atg ttt gag atg cca ttt acg cag Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln 740 745 750	2255
acc ggg aag agg cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr 755 760 765	2303
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gat gat aca aac aca aag cga tat cct gac aat aaa gtg aag ctg ctt	2591

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		850					855					860				
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Lys	Glu	Val	Phe	Arg	Gln	Phe	Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	
		865				870					875					
gta	aac	gaa	cgt	ctg	att	aaa	gaa	gac	cag	ctc	gag	tat	cag	gaa	gaa	2687
Val	Asn	Glu	Arg	Leu	Ile	Lys	Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	
		880				885				890					895	
atg	aaa	gcc	aac	tac	agg	gaa	atg	gcg	aag	gag	ctt	tct	gaa	atc	atg	2735
Met	Lys	Ala	Asn	Tyr	Arg	Glu	Met	Ala	Lys	Glu	Leu	Ser	Glu	Ile	Met	
				900					905						910	
cat	gag	cag	atc	tgc	ccc	ctg	gag	gag	aag	acg	agc	gtc	tta	ccg	aat	2783
His	Glu	Gln	Ile	Cys	Pro	Leu	Glu	Glu	Lys	Thr	Ser	Val	Leu	Pro	Asn	
			915					920					925			
tcc	ctt	cac	atc	ttc	aac	gcc	atc	agt	ggg	act	cca	aca	agc	aca	atg	2831
Ser	Leu	His	Ile	Phe	Asn	Ala	Ile	Ser	Gly	Thr	Pro	Thr	Ser	Thr	Met	
		930					935					940				
gtt	cac	ggg	atg	acc	agc	tcg	tct	tcg	gtc	gtg	tgattacatc	tcattggcccg				2884
Val	His	Gly	Met	Thr	Ser	Ser	Ser	Ser	Val	Val						
		945					950									
tgtgtgggga	cttgctttgt	catttgcaaa	ctcaggatgc	tttccaaagc	caatcactgg											2944
ggagaccgag	cacagggagg	accaagggga	aggggagaga	aaggaaataa	agaacaacgt											3004
tattttcttaa	cagactttct	ataggagttg	taagaaggtg	cacatatttt	tttaaattctc											3064
actggcaata	ttcaaagttt	tcattgtgtc	ttaacaaagg	tgtggtagac	actcttgagc											3124
tggacttaga	ttttattctt	ccttgccagag	tagtgttaga	atagatggcc	tacagaaaaa											3184
aaaggttctg	ggatctacat	ggcagggagg	gctgcactga	cattgatgcc	tgggggacct											3244
tttgccctcga	ctcgtgccgg	aaatctgac	gtaatcaggg	tacagaactt	actagttttg											3304
tctaggagta	tgttgtatga	ctaggatttg	tgctattatc	tcattcaaca	acatagagca											3364
agaatagtga	gctaactgag	ctagacactc	aattaatccg	ctactggctt	caagtcagaa											3424
ctttgtcatt	aatcatcgac	tccgggacgg	tcatatatgt	attacatttc	tacattttta											3484
atactcacat	gggcttatgc	attaagttta	attgtgataa	atttgtgctg	gtccagtata											3544
tgcaatacac	tttaatgggt	tattcttgct	ataaaaatgt	gcaatatgga	gatgtatata											3604
agtctttact																3614

<210> 17

<211> 954

<212> PRT

<213> Homo sapiens

<223> Human cadherin-like asymmetry protein 2A-80
(CLASP-2A-80)

<400> 17
 Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu
 1 5 10 15
 Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg
 20 25 30
 Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys
 35 40 45
 His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile
 50 55 60
 Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln
 65 70 75 80
 Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met
 85 90 95
 Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val
 100 105 110
 Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu
 115 120 125
 Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro
 130 135 140
 Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser
 145 150 155 160
 Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn
 165 170 175
 Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val
 180 185 190
 Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys
 195 200 205
 Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr
 210 215 220
 Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
 225 230 235 240
 Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala
 245 250 255
 Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln
 260 265 270
 Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu
 275 280 285
 Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr
 290 295 300
 Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn
 305 310 315 320

Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe
 325 330 335
 Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro
 340 345 350
 Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His
 355 360 365
 Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu
 370 375 380
 Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys
 385 390 395 400
 Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser
 405 410 415
 Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn
 420 425 430
 Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln
 435 440 445
 Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly
 450 455 460
 Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn
 465 470 475 480
 Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp
 485 490 495
 Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys
 500 505 510
 Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu
 515 520 525
 Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp
 530 535 540
 Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala
 545 550 555 560
 Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg
 565 570 575
 Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro
 580 585 590
 Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp
 595 600 605
 Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala
 610 615 620
 Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr
 625 630 635 640
 Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp

<210> 18
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(525)

<220>
 <223> Human cadherin-like asymmetry protein 2F
 (CLASP-2F)

<400> 18
 gct gat tcg aga gga tct ctc ata agc aca gat tcg ggt aac agc ctt 48
 Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu
 1 5 10 15
 cca gaa agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa 96
 Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
 20 25 30
 agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag 144
 Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
 35 40 45
 tct gag att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc 192
 Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
 50 55 60
 atg tct gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct 240
 Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
 65 70 75 80
 gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc 288
 Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
 85 90 95
 cag tac atg ggg aag cga tac ata gcc agt gtg aga aag ata tca agt 336
 Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
 100 105 110
 gtg ctt gga att tct gta gac aat ggc tat ggc cac tcg gac gca gat 384
 Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
 115 120 125
 gtt ctg cac cag tca tta ctt gaa gcc aac att gct act gag gtt tgc 432
 Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
 130 135 140
 ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac 480
 Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
 145 150 155 160
 cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa aaa aaa a 526
 Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
 165 170 175

<210> 19
 <211> 175

<212> PRT
 <213> Homo sapiens
 <223> Human cadherin-like asymmetry protein 2F
 (CLASP-2F)

<400> 19
 Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu
 1 5 10 15
 Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
 20 25 30
 Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
 35 40 45
 Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
 50 55 60
 Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
 65 70 75 80
 Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
 85 90 95
 Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
 100 105 110
 Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
 115 120 125
 Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
 130 135 140
 Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
 145 150 155 160
 Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
 165 170 175

<210> 20
 <211> 738
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> Rat TRG protein

<400> 20
 Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
 1 5 10 15
 Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
 20 25 30
 Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
 35 40 45
 Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
 50 55 60

Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
 65 70 75 80
 Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
 85 90 95
 Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
 100 105 110
 Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
 115 120 125
 Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
 130 135 140
 Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
 145 150 155 160
 Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
 165 170 175
 Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
 180 185 190
 Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
 195 200 205
 Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala
 210 215 220
 Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln
 225 230 235 240
 Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys
 245 250 255
 Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 260 265 270
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 275 280 285
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 290 295 300
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu
 305 310 315 320
 Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu
 325 330 335
 Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val
 340 345 350
 Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly
 355 360 365
 Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 370 375 380

Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 385 390 395 400
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 405 410 415
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe
 420 425 430
 Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
 435 440 445
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg
 450 455 460
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 465 470 475 480
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 485 490 495
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 500 505 510
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 515 520 525
 Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr

705		710		715		720									
Val	Ile	Phe	Asn	Ser	Arg	Phe	Tyr	Arg	Ser	Trp	Gly	Lys	Val	His	Ile
			725						730					735	

Phe Phe

<210> 21
 <211> 1214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Human CLASP-4 protein

<400> 21
 Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
 1 5 10 15
 Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
 20 25 30
 Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
 35 40 45
 Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
 50 55 60
 Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65 70 75 80
 Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
 85 90 95
 Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
 100 105 110
 Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
 115 120 125
 Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
 130 135 140
 Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
 145 150 155 160
 Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
 165 170 175
 Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
 180 185 190
 Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
 195 200 205
 Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220
 Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser

225		230		235		240									
Asn	Leu	Glu	Tyr	Ser	Leu	Ser	Asp	Glu	Tyr	Cys	Lys	His	His	Phe	Leu
				245					250					255	
Val	Gly	Leu	Leu	Leu	Arg	Glu	Thr	Ser	Ile	Ala	Leu	Gln	Asp	Asn	Tyr
		260						265					270		
Glu	Ile	Arg	Tyr	Thr	Ala	Ile	Ser	Val	Ile	Lys	Asn	Leu	Leu	Ile	Lys
		275					280					285			
His	Ala	Phe	Asp	Thr	Arg	Tyr	Gln	His	Lys	Asn	Gln	Gln	Ala	Lys	Ile
	290					295					300				
Ala	Gln	Leu	Tyr	Leu	Pro	Phe	Val	Gly	Leu	Leu	Leu	Glu	Asn	Ile	Gln
305					310					315					320
Arg	Leu	Ala	Gly	Arg	Asp	Thr	Leu	Tyr	Ser	Cys	Ala	Ala	Met	Pro	Asn
				325					330					335	
Ser	Ala	Ser	Arg	Asp	Glu	Phe	Pro	Cys	Gly	Phe	Thr	Ser	Pro	Ala	Asn
			340					345					350		
Arg	Gly	Ser	Leu	Ser	Thr	Asp	Lys	Asp	Thr	Ala	Tyr	Gly	Ser	Phe	Gln
		355					360					365			
Asn	Gly	His	Gly	Ile	Lys	Arg	Glu	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Pro
	370					375					380				
Glu	Gly	Ala	Thr	Gly	Phe	Pro	Asp	Gln	Gly	Asn	Thr	Gly	Glu	Asn	Thr
385					390					395					400
Arg	Gln	Ser	Ser	Thr	Arg	Ser	Ser	Val	Ser	Gln	Tyr	Asn	Arg	Leu	Asp
				405					410					415	
Gln	Tyr	Glu	Ile	Arg	Ser	Leu	Leu	Met	Cys	Tyr	Leu	Tyr	Ile	Val	Lys
		420						425					430		
Met	Ile	Ser	Glu	Asp	Thr	Leu	Leu	Thr	Tyr	Trp	Asn	Lys	Val	Ser	Pro
		435					440					445			
Gln	Glu	Leu	Ile	Asn	Ile	Leu	Ile	Leu	Leu	Glu	Val	Cys	Leu	Phe	His
	450					455					460				
Phe	Arg	Tyr	Met	Gly	Lys	Arg	Asn	Ile	Ala	Arg	Val	His	Asp	Ala	Trp
465					470					475					480
Leu	Ser	Lys	His	Phe	Gly	Ile	Asp	Arg	Lys	Ser	Gln	Thr	Met	Pro	Ala
				485				490						495	
Leu	Arg	Asn	Arg	Ser	Gly	Val	Met	Gln	Ala	Arg	Leu	Gln	His	Leu	Ser
			500					505					510		
Ser	Leu	Glu	Ser	Ser	Phe	Thr	Leu	Asn	His	Ser	Ser	Thr	Thr	Thr	Glu
		515					520					525			
Ala	Asp	Ile	Phe	His	Gln	Ala	Leu	Leu	Glu	Gly	Asn	Thr	Ala	Thr	Glu
	530					535					540				
Val	Ser	Leu	Thr	Val	Leu	Asp	Thr	Ile	Ser	Phe	Phe	Thr	Gln	Cys	Phe
545					550					555					560

Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605
 Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620
 Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640
 Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655
 Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670
 Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685
 Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro
 690 695 700
 Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg
 705 710 715 720
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys
 725 730 735
 Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 740 745 750
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys
 755 760 765
 Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val
 770 775 780
 His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe
 785 790 795 800
 Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu
 805 810 815
 Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser
 820 825 830
 Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp
 835 840 845
 Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly
 850 855 860
 Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr
 865 870 875 880

Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr
 885 890 895
 Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln
 900 905 910
 Ser Phe Phe Glu Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 915 920 925
 Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr
 930 935 940
 Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp
 945 950 955 960
 Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
 965 970 975
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
 980 985 990
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
 995 1000 1005
 Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
 1185 1190 1195 1200
 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val

1205

1210

<210> 22

<211> 1288

<212> PRT

<213> Homo sapiens

<220>

<223> Human CLASP-1 protein

<400> 22

Met Ser Phe Leu Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val
 1 5 10 15

Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
 20 25 30

Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45

Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60

Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
 65 70 75 80

Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
 85 90 95

Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
 100 105 110

Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
 115 120 125

Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
 130 135 140

Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
 145 150 155 160

Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
 165 170 175

Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
 180 185 190

Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
 195 200 205

His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
 210 215 220

Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
 225 230 235 240

Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
 245 250 255

Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp

260					265					270					
Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys	Asn	Leu	Met	Ala	Lys	His
		275					280					285			
Ser	Phe	Asp	Asp	Arg	Tyr	Arg	Glu	Pro	Arg	Lys	Gln	Ala	Gln	Ile	Ala
	290					295					300				
Ser	Leu	Tyr	Met	Pro	Leu	Tyr	Gly	Met	Leu	Leu	Asp	Asn	Met	Pro	Arg
	305					310					315				320
Ile	Tyr	Leu	Lys	Asp	Leu	Tyr	Pro	Phe	Thr	Val	Asn	Thr	Ser	Asn	Gln
				325					330					335	
Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr
			340					345					350		
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val
		355					360					365			
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn
	370					375					380				
His	Ala	Asp	Ser	Arg	Ala	Ser	Leu	Ala	Ser	Leu	Asp	Ser	Asn	Pro	Ser
	385					390					395				400
Thr	Asn	Glu	Lys	Ser	Ser	Glu	Lys	Thr	Asp	Asn	Cys	Glu	Lys	Ile	Pro
				405					410					415	
Arg	Pro	Leu	Ala	Leu	Ile	Gly	Ser	Thr	Leu	Arg	Phe	Asp	Arg	Leu	Asp
			420					425					430		
Gln	Ala	Glu	Thr	Arg	Ser	Leu	Leu	Met	Cys	Phe	Leu	His	Ile	Met	Lys
		435					440					445			
Thr	Ile	Ser	Tyr	Glu	Thr	Leu	Ile	Ala	Tyr	Trp	Gln	Arg	Ala	Pro	Ser
	450					455					460				
Pro	Glu	Val	Ser	Asp	Phe	Phe	Ser	Ile	Leu	Asp	Val	Cys	Leu	Gln	Asn
	465					470					475				480
Phe	Arg	Tyr	Leu	Gly	Lys	Arg	Asn	Ile	Ile	Arg	Lys	Ile	Ala	Ala	Ala
				485					490					495	
Phe	Lys	Phe	Val	Gln	Ser	Thr	Gln	Asn	Asn	Gly	Thr	Leu	Lys	Gly	Ser
			500					505					510		
Asn	Pro	Ser	Cys	Gln	Thr	Ser	Gly	Leu	Leu	Ala	Gln	Trp	Met	His	Ser
		515					520					525			
Thr	Ser	Arg	His	Glu	Gly	His	Lys	Gln	His	Arg	Ser	Gln	Thr	Leu	Pro
	530					535						540			
Ile	Ile	Arg	Gly	Lys	Asn	Ala	Leu	Ser	Asn	Pro	Lys	Leu	Leu	Gln	Met
	545					550					555				560
Leu	Asp	Asn	Thr	Met	Thr	Ser	Asn	Ser	Asn	Glu	Ile	Asp	Ile	Val	His
				565					570					575	
His	Val	Asp	Thr	Glu	Ala	Asn	Ile	Ala	Thr	Glu	Gly	Cys	Leu	Thr	Ile
				580				585					590		

Leu Asp Leu Val Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln
 595 600 605
 Gln Cys Asp Cys Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr
 610 615 620
 Met Leu Phe Phe Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val
 625 630 635 640
 Phe Ala Ser Leu Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe
 645 650 655
 Gln Gly Pro Ala Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys
 660 665 670
 Cys Cys Asn His Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu
 675 680 685
 Leu Tyr Leu Phe Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser
 690 695 700
 Ile Val Arg Ser His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile
 705 710 715 720
 Ala Asp Ala Gly Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile
 725 730 735
 Thr Asn Asn Phe Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe
 740 745 750
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 755 760 765
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val
 770 775 780
 Asp Leu Gln Tyr Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu
 785 790 795 800
 Arg Arg Thr Trp Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly
 805 810 815
 Asp Leu Ser Glu Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile
 820 825 830
 Ala Glu Tyr Leu Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys
 835 840 845
 Thr Ala Ser Leu Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser
 850 855 860
 Leu Leu Thr Thr Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro
 865 870 875 880
 Ala Phe Leu Ser Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys
 885 890 895
 Glu Asp Ser Gly Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val
 900 905 910

Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
 915 920 925
 Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
 930 935 940
 Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
 945 950 955 960
 Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
 965 970 975
 Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
 980 985 990
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
 995 1000 1005
 Ser Glu Ile Ser Gln Arg Leu Lys Leu Tyr Ala Asp Lys Phe Gly
 1010 1015 1020
 Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055
 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070
 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085
 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135
 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150
 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180
 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200
 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215
 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230
 Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn

1235 1240 1245
 Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260
 Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280
 Ser Ile Ser Ser Ser Ala Glu Val
 1285

 <210> 23
 <211> 1220
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Human CLASP-3 protein

 <400> 23
 Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
 1 5 10 15
 Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
 20 25 30
 Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
 35 40 45
 Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
 50 55 60
 Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
 65 70 75 80
 Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
 85 90 95
 Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
 100 105 110
 Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
 115 120 125
 Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
 130 135 140
 Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
 145 150 155 160
 Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
 165 170 175
 Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
 180 185 190
 Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
 195 200 205
 Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys

210	215	220
Ser Cys Tyr Lys Gln Val	Ser Ser Lys Leu Tyr	Ser Leu Pro Asn Pro
225	230	235 240
Ser Val Leu Val Ser	Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser	
	245	250 255
His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro		
	260	265 270
Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser		
	275	280 285
Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu		
	290	295 300
Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu		
	305	310 315 320
Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly		
	325	330 335
Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His		
	340	345 350
Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala		
	355	360 365
Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln		
	370	375 380
Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys		
	385	390 395 400
Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln		
	405	410 415
Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg		
	420	425 430
Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr		
	435	440 445
Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val		
	450	455 460
Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu		
	465	470 475 480
Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val		
	485	490 495
Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser		
	500	505 510
Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala		
	515	520 525
Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg		
	530	535 540

Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu
 545 550 555 560
 Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu
 565 570 575
 Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp
 580 585 590
 Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu
 595 600 605
 Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu
 610 615 620
 Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser
 625 630 635 640
 Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser
 645 650 655
 Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp
 660 665 670
 Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile
 675 680 685
 Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe
 690 695 700
 Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser
 705 710 715 720
 Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu
 725 730 735
 Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu
 740 745 750
 Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn
 755 760 765
 Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu
 770 775 780
 Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr
 785 790 795 800
 Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly
 805 810 815
 Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val
 820 825 830
 His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg
 835 840 845
 Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn
 850 855 860

Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu
 865 870 875 880
 Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly
 885 890 895
 Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu
 900 905 910
 Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
 915 920 925
 Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
 930 935 940
 Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
 945 950 955 960
 Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990
 Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys

1185 1190 1195 1200
 Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
 1205 1210 1215
 Leu Ser Ser Pro
 1220

 <210> 24
 <211> 987
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> Human CLASP-5 protein

 <400> 24
 Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
 1 5 10 15
 Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
 20 25 30
 Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
 35 40 45
 Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
 50 55 60
 Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
 65 70 75 80
 Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
 85 90 95
 Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
 100 105 110
 Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
 115 120 125
 Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
 130 135 140
 Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
 145 150 155 160
 Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
 165 170 175
 Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
 180 185 190
 Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
 195 200 205
 Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
 210 215 220
 Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln

225		230		235		240
Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu						
		245		250		255
Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro						
		260		265		270
Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys						
		275		280		285
Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys						
		290		295		300
Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu						
305		310		315		320
Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser						
		325		330		335
Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val						
		340		345		350
Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His						
		355		360		365
Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu						
		370		375		380
Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu						
385		390		395		400
His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala						
		405		410		415
Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe						
		420		425		430
Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly						
		435		440		445
Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr						
		450		455		460
Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe						
465		470		475		480
Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr						
		485		490		495
Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met						
		500		505		510
Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu						
		515		520		525
Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys						
		530		535		540
Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val						
545		550		555		560

Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
 565 570 575
 Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
 580 585 590
 Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
 595 600 605
 Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
 610 615 620
 Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
 625 630 635 640
 Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
 645 650 655
 Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
 660 665 670
 Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
 675 680 685
 Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
 690 695 700
 Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
 705 710 715 720
 Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
 725 730 735
 Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 740 745 750
 Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
 755 760 765
 Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
 770 775 780
 Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
 785 790 795 800
 Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
 805 810 815
 Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
 820 825 830
 Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 835 840 845
 Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
 850 855 860
 Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
 865 870 875 880

Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
885 890 895

His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
900 905 910

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
915 920 925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
930 935 940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
945 950 955 960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
965 970 975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
980 985

<210> 25
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-1

<400> 25
Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
1 5 10 15
Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 26
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-2D KIAA1058

<400> 26
Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
1 5 10 15
Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
20 25 30
Tyr Ile Tyr Lys Glu Pro
35

<210> 27
<211> 14

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motif B from CLASP-2

<400> 27
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 1 5 10

<210> 28
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from CLASP-6

<400> 28
 Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
 1 5 10 15
 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 29
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from CLASP-4

<400> 29
 Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
 1 5 10 15
 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 30
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from DOCK180

<400> 30
 Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
 1 5 10 15
 Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
 20 25 30

<210> 31
 <211> 31
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from DOCK2

 <400> 31
 Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
 1 5 10 15
 Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
 20 25 30

<210> 32
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from DOCK3

 <400> 32
 Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
 1 5 10 15
 Lys Glu Tyr Val Cys Arg Gly His
 20

<210> 33
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from KIAA0716

 <400> 33
 Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
 1 5 10 15
 Lys Glu Phe Val Cys Arg Gly His
 20

<210> 34
 <211> 23
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs A and B from CLASP-3

<400> 34

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 35

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from rat TRG

<400> 35

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45

Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 36

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-1

<400> 36

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 37

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-2

<400> 37

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 38

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-4

<400> 38

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
50 55 60

<210> 39

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from CLASP-3

<400> 39

Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
50 55 60

<210> 40
 <211> 54
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motif C from KIAA0716

 <400> 40
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
 1 5 10 15

 Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
 20 25 30

 Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45

 Ile Pro Glu Ser Gln Glu
 50

<210> 41
 <211> 54
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motif C from DOCK3

 <400> 41
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
 1 5 10 15

 Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
 20 25 30

 Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45

 Ile Pro Asp Tyr Val Asp
 50

<210> 42
 <211> 46
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motif C from DOCK2

 <400> 42
 Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
 1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
35 40 45

<210> 43

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motif C from DOCK180

<400> 43

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
35 40 45

Leu Asp Glu His Pro
50

<210> 44

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from CLASP-1

<400> 44

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
35 40 45

<210> 45

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from rat TRG

<400> 45

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg

1 5 10 15
 Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
 35 40 45

<210> 46

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-2D KIAA1058

<400> 46

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 47

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-2

<400> 47

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
 35 40 45

<210> 48

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from CLASP-6

<400> 48

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15

Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40

<210> 49

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from CLASP-4

<400> 49

Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
20 25 30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
35 40 45

<210> 50

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from CLASP-3

<400> 50

Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
20 25 30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
35 40 45

<210> 51

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from CLASP-5

<400> 51

Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15

Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
20 25 30

Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
35 40 45

<210> 52
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from KIAA0716

<400> 52
Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
35 40 45

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from DOCK2

<400> 53
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
1 5 10 15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
20 25 30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
35 40 45

<210> 54
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs D and E from DOCK3

<400> 54
Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
1 5 10 15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn

20 25 30
 Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

 <210> 55
 <211> 45
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs D and E from DOCK180

 <400> 55
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

 <210> 56
 <211> 58
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from CLASP-1

 <400> 56
 Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15
 Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30
 Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
 35 40 45
 Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

 <210> 57
 <211> 58
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from rat TRG

 <400> 57
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 58

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-2D KIAA1058

<400> 58

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 59

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-2

<400> 59

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 60

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-6

<400> 60

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 61

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-3

<400> 61

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 62

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-4

<400> 62

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
50 55

<210> 63
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from CLASP-5

<400> 63
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15
Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30
Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45
Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

<210> 64
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from KIAA0716

<400> 64
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15
Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30
Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45
Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 65
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs F and G from DOCK2

<400> 65
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly

1 5 10 15
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30
 Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45
 Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 66
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from DOCK3

<400> 66
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15
 Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30
 Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45
 Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 67
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP/DOCK
 motifs F and G from DOCK180

<400> 67
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30
 Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45
 Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
 50 55 60

<210> 68
 <211> 683
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 1.1
sequence of bacterial artificial chromosome BAC4
using primer HC2AS2

<220>

<221> modified_base

<222> (1)..(683)

<223> n is g, a, c, or t

<400> 68

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tttctacagn gtntactcag gtatgtgctc cttcaacaaa attagcagtt gctgctctgt 60
gacaaagttt gcaccatttt gcaagaagaa aaaaatccta atgtgttata ttactatatt 120
tttactctat agatcttttt ctaaagaaaag aaagtacaac tgaagtgcctt atatgtattc 180
atataaatga ctagtacaag catcattttg caacagattt cccctttcat tggaggatct 240
tcttgatgtt atttgtacac gatcaatttt tagtcttaat aagatgaggc tgggtgtggt 300
ggctcacacc tgtaatccta gcatttttga ggccaaggtg ggcagatcac tttagcccag 360
gggtttgaga ccagcctggc caacatggca aaaccttgct tctacaaaaa tacnaaaatt 420
atccaggcat ggtgatgtgt gctgttagtc ccaactncct aggaggctag gggtaggggg 480
atttgaaga ggctgggagg gtcaaagccc naantgagcc attggtncat gtcacttgga 540
ccccaagcnn gggnganca agagcaaag actnntgttn tttanaaaaa aaaccgggct 600
accatacnna ccaaccncn nacctaccn acctttccan nttaaaanaa ggctttgnct 660
tgcanaaggaa aancaaaatn ncc 683
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<210> 69

<211> 673

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 1.2
sequence of bacterial artificial chromosome BAC26
using primer HC2AS2

<220>

<221> modified_base

<222> (1)..(673)

<223> n = g, a, c, or t

<400> 69

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tctggtttct acagtgtata ctnaggtatg tgctccttna acaaaattag cagttgctgc 60
tctgtgacaa agtttgcacc attttgcaag aagaaaaaaa tcctaattgtg ttatattact 120
atatttttac tctatagatc tttttctaaa gaaagaaagt acaactgaag tgcttatatg 180
tattcatata aatgactagt acaagcatca ttttgcaaca gatttcccct ttcatgggag 240
gatcttcttg atgttatgtg tacacgatca atttttagtc ttaataagat gaggctgggt 300
gtggtggctc acacctgtaa tcctagcatt ttggaggcca aggtgggcag atcactttag 360
cccaggggtt tgagaccagc ctggccaaca tggcaaaacc ttgtctctac aaaaatacaa 420
aaattatcca ggcatggtga tgtgtgcctg tagtcccagc tacctaggag gctagggtag 480
ggggattgca agaggctnng aggtcaaggc cgcagtgag ccatggtcac gtcactgcac 540
cccagccag ggccgacagg agcaagactn ttgnttcaaa aaaaaacagn aaccaacanc 600
caacaacaac aacnaccttt cngcaaaaana agcttgctnc aangaaacca aaatgncttc 660
ttnttttccc ccn 673
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<210> 70

<211> 1034

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 1.3
sequence of bacterial artificial chromosome BAC6
using primer HC2AS2

<220>

<221> modified_base

<222> (1)..(1034)

<223> n = g, a, c, or t

<400> 70

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agnnnnnccc nctacnccac ttttaacctt ttgaaaacac agtgtttntct caantatgcg 60
ctccttcaca tattagcagt tgctgctctg tgacatagtt gcaccattnt gcaagaagaa 120
aaaatcctaa gtgtnatata actatatnnn tactctatag atcttntcta aagaaagaaa 180
gtcaactgat gtgcttatat gtatncatat aaatgactag tacatgcata attttgcaac 240
agatntctcc tcacattgga ggatcttctn gangnattcg acacgatnan tattagtctn 300
aataagatga ngctgggtgtg gnggtacact gnatctagca tntggangca tgtggcagac 360
acttanccnc ggtngagaca gctgtcactg ncnactgtc tctntaaanc aaannctccg 420
cngnggatgg gctgagccag tectagnngc tagntägnä tgnngagntg tngcacngcg 480
agngagcattg ntctgtactg actcatcagg cgncnacacg ntctgttcna aaacatacca 540
cacacactcn cactcnogca aaattgctct nnaaanatgc ttntttcaca cngntncaat 600
cncatatnnt tcttctattc tncnactnt nattannatc ttncnctgca naacnatnng 660
nccacctnna nnaccttang cttngtttca cgcttatagc tcccctacac ntncacgcn 720
ttncnngtga agggccnccc gaactctacga ncatactctc tccgtatatn gcctcggta 780
ncgcatctg ctgtnntctc ntcnctngcn nttnancngt ncgctatctc tnnnccgat 840
ccncccata tnnntnctct acttanagcg taanntntnc ncncactant cacaactnt 900
ncntnnaact ctatctnctc ctctctacca cctcacttac tacctnttca cncantctcc 960
ttcnctntcc actgatctcc acatagctgc tntactgcc antttatcat atncacacnc 1020
tctacgctnn ntnt 1034
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<210> 71

<211> 644

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 2.1
sequence of bacterial artificial chromosome BAC4
using primer HC2S1

<220>

<221> modified_base

<222> (1)..(644)

<223> n = g, a, c, or t

<400> 71

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cttgatttna aagagggtct gcaggaagaa gtgtgtagtc ataaatacct cactggatat 60
tttatacagg attctaaaaa acctattagc aatagtatgc tagaaatagt cattagcttc 120
ttgaccttct tagaactgca cactctattg cactgtacag atttcaggat ggctgcaggg 180
attgatttga aaactaagga cacatttcaa taaacaatgt cttcaattga tttttagggc 240
tcctctact tcaatgaagg acttcaggta gcttataatt acagacacag gctcaataca 300
ataaaaaaat tagtaaggca gagctttaa aaaaaaaaag gaaaaagata attctaccag 360
agaaaggcta catggtgact tctgttacca gtaacaaccc ccgcactacc tttgggtctc 420
caggagcaaa acagctaatt tagttgttga tctgcttgaa gacaaagccc ctgtccatga 480
aggtgaaaca tctctgtgga ggaaaacaag caaaaaagtt atttcaggtc caaacatttc 540
ggaaatttgg attcaaagca ggcatattt gctaataagt ttatccactg acataaaaaa 600
catgccttca acattgccag agcacctact ctatntagt cncn 644
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<210> 72
 <211> 725
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 3.1
 sequence of bacterial artificial chromosome BAC4
 using primer C96AS

<220>
 <221> modified_base
 <222> (1)..(725)
 <223> n = g, a, c, or t

<400> 72
 aatcagcaga ccaaacagag gcaggtagag ggtggctatc cttgcctgat ggctctgaaa 60
 agaagacaca catggtaagt ttgaccagag attctgagaa ccgaactaag ttggtgctga 120
 ccatctcctt tatttgatc ctctctataa agacagatat ttgatttttag tcccaaaata 180
 gagcaaaatc ttagtgctgt taccatgaat tttctaactg .attactttct ttacaccact 240
 taaaataaag gacattatca atgcacattc ctccattgg ggaccactca cccttgaagc 300
 atatctgtca tcaaaagaat gctttatcag cagggttctg agcacactga tggcgatcag 360
 acggacctcc cggaactcct ggagggtgtg cccacacctc ctnagtaaca gtcccaccaa 420
 gaagtgggtt ctgcagaact catctgttaa tgagtagtca agctgggagg tctgaaatga 480
 ggatagaaac tactttgngt taggaaagat gcaatgctct tttgaataaa acaaacaaac 540
 caaacnaaca aaaaaaaaaa taagacccat ccttntgnat ttcaagccca ccctggggtn 600
 ggtcaaagag atgatcagna ntttggcatt naaatgaaga aagaaatnaa ttntccaggg 660
 gntgttctnc tttttagcac anggagggat nttaantgaa aaccaattta aatccaattn 720
 agng 725

<210> 73
 <211> 689
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 4.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2AS5

<220>
 <221> modified_base
 <222> (1)..(689)
 <223> n = g, a, c, or t

<400> 73
 ttcttttctg caaggctgtt cccgaatctg tgcttatgag agatcctctc gaatcagcat 60
 ttctcacact gttgatgtt ggagttgagg ttgtatatgg agaagctaaa tggaaatcaa 120
 gccacaata agtttttatt aagacagaac aaaataaaga tgagtactga actttaaggg 180
 aaattgcttt tattgcactt attttttctg ttaggaagtt ggctcaagag ttgcattcca 240
 ttacttcacc tttaaagaac caggtcatat acaatgagat aaaaagaaac tagtctgaaa 300
 cattcagatg taaacatcaa ttacttgtt agaaaccacc tttgatcgct aaagactaaa 360
 tgcatacctg tttcagaatg tgatagaatg aagacttaaa aaaattaaaa gataaatcca 420
 cctacaacta tcaaatcaca aaattaaacc acacaacaaa cttgtagcat tcaactgggt 480
 aataaacact gaggagccta cccaactctg aggggtgtca tgggggtattt taaattttcg 540
 aggagaacac agtgatatgt gacctcagcc agaagctgct gtttnagcag cagggttggtg 600
 ctatgctcct ttttgaagac atatttgtga agctgggtat tttggggggc ctgcttatga 660
 taaaanggca aggtnttcaa tgnaggggn 689

<210> 74
 <211> 680
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 4.2
 sequence of bacterial artificial chromosome BAC26
 using primer C2AS5

<220>
 <221> modified_base
 <222> (1)..(680)
 <223> n = a, g, c, or t

<400> 74
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 agccaacaat aaagttttat taagacagaa caaaataaag atgagtactg aactttaagg 180
 gaaattgctt ttattgcact tattttttct gttaggaagt tggctcaaga gttgcattcc 240
 attacttcac ctttaaagaa ccaggtcata tacaatgaga taaaaagaaa ctagtctgaa 300
 acattcagat gtaaacaatca attcacttgt tagaaaccac ctttgatcgc taaagactaa 360
 atgcatacct gtttcagaat gtgatagaat gaagacttaa aaaaattaaa agataaatcc 420
 acctacaact atcaaatcac aaaattaaac cncacaacaa acttgtagca ttcaaactgg 480
 taataaaaca ctgaggagcc taccacaact tgaggggtgt caatggggtg tttttaaat 540
 tttcgnggga nanccagtg ntatggtgac cttcacccaa gaagcttggt tgtttnacca 600
 agcnaggttg nncntgctc ctttttagaa nacnntat tnnnaaatnc tggntttttt 660
 nngnggcccc ctncnttnt 680

<210> 75
 <211> 686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 5.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S6

<220>
 <221> modified_base
 <222> (1)..(686)
 <223> n = g, c, a, or t

<400> 75
 ttcttgata aggtaattgc ttttacccaa cacaaatgtt tcttataatc aatggattta 60
 gcccaaagta aacgtacttc atgttctagt gccttttaag tgtgacctt tgtttttttc 120
 taaaccaccc ggctgacctg gagtaggtga tgagagcttt aaggttgagg ccatttcctt 180
 gaagtgcctt gattcctgtt tccagtagct cagatcctgg gcagggtttg cagtggagcg 240
 tcttgagtga atggctctgg tgggttgaac ggggaggggac tcaaaatgct gcccatctca 300
 atttctgtga gtctttttat ttattttatt attttttgag acagagtctc gctctgtcgc 360
 ccaggctgga gtacagcggc acgatctcaa ttnactgcaa cctccgcctc ctgggttcaa 420
 acgactcctc tgcctcagcc tccccagcag ctgggaccac aggcacaagc caccaccgcc 480
 cggctaattt tttgtntttt tagtagagat ggggtttcac catatttggc caggctgggc 540
 tcaaactcct gacctcgtca tccgcncctc cggncncca aagtgcttgg gattncaggc 600
 ngtgagccca cttacacctn gggcaattcc ctgtnagtct tttttaccag agacaccatc 660
 attcaacaca gcttttccac ccacaa 686

<210> 76

<211> 672
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 5.2
 sequence of bacterial artificial chromosome BAC26
 using primer C2S6

<220>
 <221> modified_base
 <222> (1)..(672)
 <223> n = g, a, c, or t

```
<400> 76
tgagaagagc aatttcctgg ataaggtaat tgcttttacc caacacaaat gtttcttata 60
atcaatggat ttagcccaaa gtaaacgtac ttcattgttct agtgcctttt aagtgtgacc 120
ttttgttttt ttctaaacca cccggctgac ctggagtagg tgatgagagc tttaagggtg 180
gggcccattc cttgaagtgc tctgattcct gtttccagta cctcagatcc tgggcagggt 240
ttgcagtggg gcgtcttgag tgaatggctc tgggtgggtg aacggggagg gactcaaaat 300
gctgcccata tcaatttcct gtagtctttt tatttattta tttatttttt gagacagagt 360
ctcgctctgt cgcccaggct ggagtacagc ggcacgatct caattcactg caacctccgn 420
ctccctgggt tcaaacgact cctctgnctn agnctcccag cagcctggga accacaggct 480
cangccacca cgcccggcta attnttgtaa ttttnagtaa naaattgggg gttctcacca 540
tnttggccca agncttgggc ctaaaaacct tncnaccnt cgncattcnc nccccnaccn 600
tgggcncctc tcaaangngc ttggggattt ancanngcn ttaaccccc ntatcaccgt 660
ggnccttaat tt                                     672
```

<210> 77
 <211> 700
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 6.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S7

<220>
 <221> modified_base
 <222> (1)..(700)
 <223> n = g, a, c, or t

```
<400> 77
nagngngggg ttagnncggt tgaagcctgn nacgnggtgn gtgctngaac tctgtgggct 60
ttcagggtact ggggtatctg ggagcctgct gtttgcatg ctagtgcata agaccagggc 120
tttttctctc ctgtagctgc tacttatata catagctcta actgagatga ttctccagac 180
aactgatgca gagcagcaaa agcttctgcc gttctcccct tctaggagtg tctcctttct 240
ttggaaagag atcatgaggg gctagattgt aatgaagtga ggctcagtgc ttgagcacat 300
ccggtaaaaag ttccaatata ttggtcataa agtttctcat tctttatagc agttaatttc 360
tctggctcat gagttttctt agttttaatc tgacttttaa attaatgtct ccagcaccag 420
tcatatcccc agggcaaaact caaaggcatg agaggccaga ctcgggctct ggctcatagca 480
accctgtct agggccttgg tccctgcctc cgcttgtgtg ctgtggcgca ggctcctatg 540
gcccttagga aacaggacca ccctgtcgca cccctacag agaccagcca agtttgacat 600
tagatcaccg tagcaatgtn tgcaaattcc agtttcttgc taaaacagggt taagccttgc 660
agccacttta tctgtaactg gcngaggttt tgacataaaa                                     700
```

<210> 78
 <211> 676

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 7.1
sequence of bacterial artificial chromosome BAC4
using primer C2S8

<220>

<221> modified_base

<222> (1)..(676)

<223> n = g, a, c, or t

<400> 78

```
ctctcgacac gctgtttcta ttaacattgg cgtttaaggt ttgtatcaat ttgctgttcg 60
nggttctagt tttacctttc acattcattc tgcttggtta gctcagttag cacaactta 120
ctatgttgca tttttacttc agcaattatt tttgtccctg taaggaaacc attaatcttt 180
aaattccttt aatgaaatca ttccacagtg aatggcttga atgccctgaa ataaaattta 240
actggtcagt gtgtgctgcg cgcttgggta tggtggaac acggtctctg gaggcagtta 300
actcttggtc cgaaccttga ggatgggtgaa tataggcacc taatcaggca tttctgcctt 360
gaatatcttt aaatatatcc aaatgttata gcgtttaatt agatttttat gtagaaagga 420
gcaataaaca caagacacat gttttcagtt ttttatctgt tactgcatta aatgataaaa 480
acgttttga gatagaaaat gaaaggggtt tttttttgt cttgttttaa agtttttagca 540
aataatattc aagtaggtgg agatggactc ttcaccactc tcctgttttt aggaacccaa 600
tactttttca ttcttgctaa atgattactt ccatttctag catagaaaag gagaaaattg 660
gaatgagtgt ttatat                                     676
```

<210> 79

<211> 686

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 8.1
sequence of bacterial artificial chromosome BAC4
using primer C2S9

<220>

<221> modified_base

<222> (1)..(686)

<223> n = a, c, g, or t

<400> 79

```
cgctttnaaa tnccagccgc tactgcgggg cgntnaattc gaaacgtggt gttntctgtg 60
atgcctggct ctgattgtgt gggattgggc atcagtgggc gttggcagnt ggggttcagt 120
gaagcggcca tggggactga tggcaggccc ttggattgcc accgcagagc ctggcagtgt 180
ctttggtctg cattcctacc gggaagtct catttcacct cacgtgttat ctcttgaaaa 240
gcattccttt agcgggctgt gtctaccctt ccatectctc gtccaaactc cccctccttc 300
tctgttctgt ctcttccca tctcttctc ccagttctt ctctctatgt tccttctca 360
gtggtttctc ttctctgtt tgactttcca aggtcatttt gactgttctt gctcccaact 420
acaaagatac taaaatctca cctaaccact cttcttcttt cttaatgaaa gaatgttttc 480
agtccatccc aaatttgtgt ggacttcaca aaccttctct aaaatggagc cttttctctt 540
cctactcttg actagntggg aaacgctcca tgttcttggc cagaactccc tggtagtag 600
cgtcactccc actttcctgt gcagaaccaa gcctcctaga aaactccttt gcanctgagt 660
gggttgggac acgcccttn tttggg                                     686
```

<210> 80

<211> 680

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 9.1
sequence of bacterial artificial chromosome BAC4
using primer C2AS10

<220>

<221> modified_base

<222> (1)..(680)

<223> n = g, a, t, or c

<400> 80

```
tttanaccna tntatccgng tcagttanag gagtctctga gaaatttccg acagcgggtgt 60
gagtttgggt tccttgtaaa tatactcctt tccatcttca tcttcaaaga atccctgtga 120
cataaagcac aattagagct atccctgaac gtaagcccag ggcttaccac ctagggaagcg 180
ttcttttatt acaaggggga aaaaaaggaa tgggtctaaa aatccagctg aaatgggctt 240
tctgaatgag aaagaaaatg ctaataacat gaagtctagg tgcaaaggta aaggaaaaac 300
acaacattgc aaacttattc aagaatgcag tcattaagtg ttgagtgaag tgaaagattt 360
tgatacaag actaagctgt cccaggggaag tctaattggga gtcaagcctg tttcactttc 420
ccaagaagca gaactcacta naaaatgatg agcagcccac gacaggcagg ctcagaagtg 480
gacatgcctc ccttctcctg atggctncca tgcacacagg attttatggc atgaactgaa 540
gcgtttgggg gtctggagta agtttagtaa aagtttagta aagcttgat aaattgtatt 600
tttgctttac ccgatgagaa aaaaaatatt naagacctgg tagcttcaat attcaagaaa 660
aatatttttc atntcaccgc 680
```

<210> 81

<211> 619

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ref 10.1
sequence of bacterial artificial chromosome BAC4
using primer C2S11

<220>

<221> modified_base

<222> (1)..(619)

<223> n = g, a, c, or t

<400> 81

```
ngnangtgga gccnccgancc agggacaatc tnaacctnct taaactgtac tcggatnaat 60
ttggttctga aaatgtcaaa atgatacagg attctggcaa ggtattgacc atgtttggan 120
aagtttcata gcaatgtaat gttgtgatnc gattacatat natatatatt taaatgtnta 180
tagaaaaaaa cacangaaaa atattaagga ttgttggccc gtgagtggca ggtgtatntt 240
cttnctgac ctttagngct ttccattaca tgcntgacat taaaaaaanc tttatcgcc 300
aatttttgaa acatctaatt ttacaaaata attaaccgtn tggccangna tattntcatt 360
tttaggncca gctatttaga aactctgaca naaatgaggg gctgtggcct ncctnccctn 420
acttgnccct ctttcnngna tgtaccacat gaacttgncc cctctttcnn ctnaccgggt 480
ggcatgttan aggacaggtt gaaaccncan tngggcngga nttnggttna attgggacac 540
aatggtacna ngctctatng gaatngaaac tctcccnacn nncngtggncc cntggggaaa 600
atgngncnna ttcattttt 619
```

<210> 82

<211> 597

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 11.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S12

<220>
 <221> modified_base
 <222> (1)..(597)
 <223> n = g, a, c, or t

<400> 82
 agnanngttn ngcagctgca nntctggacc canaggccgc angggcacga gccnggacac 60
 gctcggcaaa gagctgtcca gagggattca gaagcttcag gactggaagg gtcttttcgag 120
 ctacgttagc caccgccaca cccatttcag ttccacattt atctagtgtc tccttttgaa 180
 tacttgggat gtttttctgt tgatctgttg gcacttcctt cttccacaag accagaagct 240
 catatccaat ctaaggtcac ttacccttct gagaatctga tgaaaatggc gtgccttatg 300
 tgcctagatg cttttgcaca cagtctaagg tgacttatgg actccaggtc cagcagccac 360
 acccagtcct gggctctccg acagggaggg acccgtcttc acacacctgt ctcaggttct 420
 agcattgggc tgcttcagcg gtctcaggct gtgagtaaag gggatgtgag cttggatcgc 480
 cccacgtgt tgncccccgg ggggcttggc cagctggcca cttnгааатg cctccttttg 540
 cccaggaaag ctactgcat ttcaatggg nttntccacg aagttcanct ttanggg 597

<210> 83
 <211> 634
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 12.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S13

<220>
 <221> modified_base
 <222> (1)..(634)
 <223> n = a, c, g, or t

<400> 83
 agnaaggtnn ctcanthaan ncagcgtgag ngttcagggt agccaggcac agcaggccgg 60
 agggcagcag gggacgtcct tgcccctggg tgacttgaga gtcgtttcca ctaacaagg 120
 ctacttgaga gcctcgtttt accaagtgat ccctgtctcc tcccccaac gtntgtgaca 180
 tttctcctga tatcagaggg ggaggaaacc tcatgatccc tgccccccgc cccatgagga 240
 ctgactgtgg ggacaaagag ccagatctca tagactaccc tgatttgta gtatttgagg 300
 aattctgggt gcctgattag aagcatcaag actcttctaa atncaaagaa gtgtggagag 360
 cagtagattt tcctataaaa ctggtgttgc tggtttctat gaaaattgga tccaaaaaaa 420
 gtccttaagt ttaccctctt aatggnatct tttgattaat ggaattcatt attttaatat 480
 agcccaatca atccaatttt tctttattgg tagcattttt atgttctctt taaaaaatc 540
 ttggnctacc tccaaaattt cacagatgtt ctctagggt tttcctcctt ttggttcaag 600
 catcccatc aangtcttgc agtccattct gggg 634

<210> 84
 <211> 567
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 13.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2S14

<220>
 <221> modified_base
 <222> (1)..(567)
 <223> n = a, g, c, or t

<400> 84
 gacttanatt tattcttcct tgcagagtag tgtagaata gatggcctac agaaaaaaaa 60
 ggttctggga tctacatggc agggagggct gcactgacat tgatgcctgg gggacctttt 120
 gcctcgaggc tgagctggaa aatcttgaaa atattttttt ttctctgtgg cacattcagg 180
 ttgaatacaa gaactatttt tgtgactatg tttttgatga cctaagggaa ctgaccattg 240
 taatttttgt accantgaac cangagattt aagtgccttt atattcattt ccttgcattt 300
 aagaaaatat gaaagcttaa ggaattatgt gagcttaaaa ctagtcaagc antttagaac 360
 caaaggccta tnttnataac cgcaactatg ctnaaaagna caaagtagta cagnatattg 420
 ntatgtacat atcatttggt aatacacncc nggcnttctg tacatatatg tattacattt 480
 ctacnttttt aatactccn tgggcttatg ccnttaaggt taanttgnga taaatttngg 540
 ctgttcngt ntatncnata cncctttt 567

<210> 85
 <211> 662
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ref 14.1
 sequence of bacterial artificial chromosome BAC4
 using primer C2AS15

<220>
 <221> modified_base
 <222> (1)..(662)
 <223> n = a, c, g, t

<400> 85
 atgagaatgt aatacatata tgtacagaat gccaggactg tattaacaat gatatgtaca 60
 taacaatata ctgtactact ttgtactttt cagcatagtt gcggttatta atataggcct 120
 ttggttctaa actgcttgac tagttttaag ctacataat tccttaagct ttcatatttt 180
 cttaaatgca aggaaatgaa tataaaagca ctaaatctcc tgggttcactg gtacaaaaat 240
 tacaatggtc agttccctta ggcatcaaaa aactagtcac aaaaatagtt cttgtattca 300
 acctgaatgt gccacaggaa aaaaaaata ttttcaagat tttccagctc agcctcgagg 360
 caaaaggccc ccaggcatca atgtcagngc agccctcctg ccatgtagat cccagaacct 420
 tttttttctg taggccatct attctaacac tactctgcag ggagaataaa atctaaagnc 480
 cagctcaaga gtgtaccac acctttgtta agacacaatg aaaactttgg atattggcag 540
 gngagattta aaaaaaatg tgccctttct taccactcct atagnaaagt ctgggttaaga 600
 aataaccggt ggtctttatt ttccctttnt ttcccttcc cttgggnctt cctggggctc 660
 gg 662

<210> 86
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: KV1.3
 inhibitor

<400> 86
 Thr Thr Asn Asn Asn Pro Asn Ser Ala Val Asn Ile Lys Lys Ile Phe
 1 5 10 15

Thr Asp Val

<210> 87
<211> 4898
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (567)..(4148)

<220>
<223> Human CLASP-2

<400> 87
aattgtaata cgactcacta tagggcgaat tgggtaccgg gccccccctc gaggtcgacg 60
gtatcgataa gcttgatata gaattcggca cgagttttac accatcacca aaaccagaa 120
ttttatgatg agattaaaat agagttgccc actcagctgc atgaaaagca ccacctgttg 180
ctcacattct tccatgtcag ctgtgacaac tcaagtaaag gaagcacgaa gaagagggat 240
gtcgttgaaa cccaagttgg ctactcctgg cttcccctcc tgaaagacgg aagggtggtg 300
acaagcgagc agcacatccc ggtctcggcg aaccttcctt cgggctatct tggctaccaa 360
gagcttgagg tgggcaggca ttatggtccg gaaattaaat gggtagatgg aggcaagcca 420
ctgctgaaaa ttccactca tctggtttct acagggatac tcaggatcag catttacata 480
attttttcca gtactgtcag aaaaccgaat ctggagccca agccttagga aacgaacttg 540
taaagtacct taagagtctg catgcg atg gaa ggc cac gtg atg atc gcc ttc 593
Met Glu Gly His Val Met Ile Ala Phe
1 5
ttg ccc act atc cta aac cag ctg ttc cga gtc ctc acc aga gcc aca 641
Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr
10 15 20 25
cag gaa gaa gtc gcg gtt aac gtg act cgg gtc att att cat gtg gtt 689
Gln Glu Glu Val Ala Val Asn Val Thr Arg Val Ile Ile His Val Val
30 35 40
gcc cag tgc cat gag gaa gga ttg gag agc cac ttg agg tca tat gtt 737
Ala Gln Cys His Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val
45 50 55
aag tac gcg tat aag gct gag cca tat gtt gcc tct gaa tac aag aca 785
Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr
60 65 70
gtg cat gaa gaa ctg acc aaa tcc atg acc acg att ctc aag cct tct 833
Val His Glu Glu Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser
75 80 85
gcc gat ttc ctc acc agc aac aaa cta ctg agg tac tca tgg ttt ttc 881

Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe	
90 95 100 105	
ttt gat gta ctg atc aaa tct atg gct cag cat ttg ata gag aac tcc	929
Phe Asp Val Leu Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser	
110 115 120	
aaa gtt aag ttg ctg cga aac cag aga ttt cct gca tcc tat cat cat	977
Lys Val Lys Leu Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His	
125 130 135	
gca gcg gaa acc gtt gta aat atg ctg atg cca cac atc act cag aag	1025
Ala Ala Glu Thr Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys	
140 145 150	
ttt gga gat aat cca gag gca tct aag aac gcg aat cat agc ctt gct	1073
Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala	
155 160 165	
gtc ttc atc aag aga tgt ttc acc ttc atg gac agg ggc ttt gtc ttc	1121
Val Phe Ile Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe	
170 175 180 185	
aag cag atc aac aac tac att agc tgt ttt gct cct gga gac cca aag	1169
Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys	
190 195 200	
acc ctc ttt gaa tac aag ttt gaa ttt ctc cgt gta gtg tgc aac cat	1217
Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His	
205 210 215	
gaa cat tat att ccg ttg aac tta cca atg cca ttt gga aaa ggc agg	1265
Glu His Tyr Ile Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg	
220 225 230	
att caa aga tac caa gac ctc cag ctt gac tac tca tta aca gat gag	1313
Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu	
235 240 245	
ttc tgc aga aac cac ttc ttg gtg gga ctg tta ctg agg gag gtg ggg	1361
Phe Cys Arg Asn His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly	
250 255 260 265	
aca gcc ctc cag gag ttc cgg gag gtc cgt ctg atc gcc atc agt gtg	1409
Thr Ala Leu Gln Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val	
270 275 280	
ctc aag aac ctg ctg ata aag cat tct ttt gat gac aga tat gct tca	1457
Leu Lys Asn Leu Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser	
285 290 295	
agg agc cat cag gca agg ata gcc acc ctc tac ctg cct ctg ttt ggt	1505
Arg Ser His Gln Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly	
300 305 310	
ctg ctg att gaa aac gtc cag cgg atc aat gtg agg gat gtg tca ccc	1553
Leu Leu Ile Glu Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro	
315 320 325	
ttc cct gtg aac gcg ggc atg acc gtg aag gat gaa tcc ctg gct cta	1601
Phe Pro Val Asn Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu	

330	335	340	345	
cca gct gtg aat ccg ctg gtg acg ccg cag aag gga agc acc ctg gac	Pro Ala Val Asn Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp	1649		
350	355	360		
aac agc ctg cac aag gac ctg ctg ggc gcc atc tcc ggc att gct tct	Asn Ser Leu His Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser	1697		
365	370	375		
cca tat aca acc tca act cca aac atc aac agt gtg aga aat gct gat	Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp	1745		
380	385	390		
tcg aga gga tct ctc ata agc aca gat tcg ggt aac agc ctt cca gaa	Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu	1793		
395	400	405		
agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa agt agc	Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser	1841		
410	415	420	425	
aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag tct gag	Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu	1889		
430	435	440		
att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc atg tct	Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser	1937		
445	450	455		
gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct gaa ctt	Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu	1985		
460	465	470		
atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc cag tac	Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr	2033		
475	480	485		
atg ggg aag cga tac ata gcc agg aac cag gag ggg ttg gga ccc ata	Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile	2081		
490	495	500	505	
gtt cat gat cga aag tct cag aca ttg cct gtt tcc cgt aac aga aca	Val His Asp Arg Lys Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr	2129		
510	515	520		
gga atg atg cat gcc aga ttg cag cag ctg ggc agc ctg gat aac tct	Gly Met Met His Ala Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser	2177		
525	530	535		
ctc act ttt aac cac agc tat ggc cac tcg gac gca gat gtt ctg cac	Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp Ala Asp Val Leu His	2225		
540	545	550		
cag tca tta ctt gaa gcc aac att gct act gag gtt tgc ctg aca gct	Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala	2273		
555	560	565		
ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac cag ctc ctg	Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu	2321		
570	575	580	585	

gcc gac cat gga cat aat cct ctc atg aaa aaa gtt ttt gat gtc tac	2369
Ala Asp His Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr	
590 595 600	
ctg tgt ttt ctt caa aaa cat cag tct gaa acg gct tta aaa aat gtc	2417
Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val	
605 610 615	
ttc act gcc tta agg tcc tta att tat aag ttt ccc tca aca ttc tat	2465
Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr	
620 625 630	
gaa ggg aga gcg gac atg tgt gcg gct ctg tgt tac gag att ctc aag	2513
Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys	
635 640 645	
tgc tgt aac tcc aag ctg agc tcc atc agg acg gag gcc tcc cag ctg	2561
Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu	
650 655 660 665	
ctc tac ttc ctg atg agg aac aac ttt gat tac act gga aag aag tcc	2609
Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser	
670 675 680	
ttt gtc cgg aca cat ttg caa gtc atc ata tct gtc agc cag ctg ata	2657
Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile	
685 690 695	
gca gac gtt gtt ggc att ggg gaa acc aga ttc cag cag tcc ctg tcc	2705
Ala Asp Val Val Gly Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser	
700 705 710	
atc atc aac aac tgt gcc aac agt gac cgg ctt att aag cac acc agc	2753
Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser	
715 720 725	
ttc tcc tct gat gtg aag gac tta acc aaa agg ata cgc acg gtg cta	2801
Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu	
730 735 740 745	
atg gcc acc gcc cag atg aag gag cat gag aac gac cca gag atg ctg	2849
Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met Leu	
750 755 760	
gtg gac ctc cag tac agc ctg gcc aaa tcc tat gcc agc acg ccc gag	2897
Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu	
765 770 775	
ctc agg aag acg tgg ctc gac agc atg gcc agg atc cat gtc aaa aat	2945
Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys Asn	
780 785 790	
ggc gat ctc tca gag gca gca atg tgc tat gtc cac gta aca gcc cta	2993
Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala Leu	
795 800 805	
gtg gca gaa tat ctc aca cgg aaa ggc gtg ttt aga caa gga tgc acc	3041
Val Ala Glu Tyr Leu Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr	
810 815 820 825	

gcc ttc agg gtc att acc cca aac atc gac gag gag gcc tcc atg atg	3089
Ala Phe Arg Val Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met	
830 835 840	
gaa gac gtg ggg atg cag gat gtc cat ttc aac gag gat gtg ctg atg	3137
Glu Asp Val Gly Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met	
845 850 855	
gag ctc ctt gag cag tgc gca gat gga ctc tgg aaa gcc gag cgc tac	3185
Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr	
860 865 870	
gag ctc atc gcc gac atc tac aaa ctt atc atc ccc att tat gag aag	3233
Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys	
875 880 885	
cgg agg gat ttc ttt gaa gat gaa gat gga aag gag tat att tac aag	3281
Arg Arg Asp Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys	
890 895 900 905	
gaa ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa	3329
Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys	
910 915 920	
ctg tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg ata cag gat	3377
Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp	
925 930 935	
tct ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc	3425
Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile	
940 945 950	
cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa	3473
Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu	
955 960 965	
agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt	3521
Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe	
970 975 980 985	
gag atg cca ttt acg cag acc ggg aag agg cag ggc ggc gtg gaa gag	3569
Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu	
990 995 1000	
cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat	3617
Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr	
1005 1010 1015	
gtg aag aag cgc atc cct gtc atg tac cag cac cac act gac ctg aac	3665
Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn	
1020 1025 1030	
ccc atc gag gtg gcc att gac gag atg agt aag aag gtg gcg gag ctc	3713
Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu	
1035 1040 1045	
cgg cag ctg tgc tcc tcg gcc gag gtg gac atg atc aaa ctg cag ctc	3761
Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu	
1050 1055 1060 1065	
aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc cca cta gca	3809

Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala
 1070 1075 1080
 tat gcg cga gct ttc tta gat gat aca aac aca aag cga tat cct gac 3857
 Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp
 1085 1090 1095
 aat aaa gtg aag ctg ctt aag gaa gtt ttc agg caa ttt gtg gaa gct 3905
 Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala
 1100 1105 1110
 tgc ggt caa gcc tta gcg gta aac gaa cgt ctg att aaa gaa gac cag 3953
 Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln
 1115 1120 1125
 ctc gag tat cag gaa gaa atg aaa gcc aac tac agg gaa atg gcg aag 4001
 Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys
 1130 1135 1140 1145
 gag ctt tct gaa atc atg cat gag cag atc tgc ccc ctg gag gag aag 4049
 Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys
 1150 1155 1160
 acg agc gtc tta ccg aat tcc ctt cac atc ttc aac gcc atc agt ggg 4097
 Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly
 1165 1170 1175
 act cca aca agc aca atg gtt cac ggg atg acc agc tcg tct tcg gtc 4145
 Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Val
 1180 1185 1190
 gtg tgattacatc tcatggcccg tgtgtgggga cttgctttgt catttgcaaa 4198
 Val
 ctcaggatgc tttccaaagc caatcactgg ggagaccgag cacagggagg accaagggga 4258
 aggggagaga aaggaaataa agaacaacgt tatttcttaa cagactttct ataggagttg 4318
 taagaaggtg cacatatattt tttaaattctc actggcaata ttcaaagttt tcattgtgtc 4378
 ttaacaaagg tgtggtagac actcttgagc tggacttaga ttttattctt ccttgagag 4438
 tagtggttaga atagatggcc tacagaaaaa aaagggttctg ggatctacat ggcagggagg 4498
 gctgcactga cattgatgcc tgggggacct tttgcctcga ctcggtgccg aaatctgatc 4558
 gtaatcaggg tacagaactt actagttttg tctaggagta tgttgtatga ctaggatttg 4618
 tgctattatc tcattcaaca acatagagca agaatagtga gctaactgag ctagacactc 4678
 aattaatccg ctactggctt caagtcagaa ctttgtcatt aatcatcgac tccgggacgg 4738
 tcatatatgt attacatttc tacattttta atactcacat gggcttatgc attaagttta 4798
 attgtgataa atttgtgtg gtccagtata tgcaatacac tttaatggtt tattcttgctc 4858
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<210> 88
 <211> 1194

<212> PRT
 <213> Homo sapiens
 <223> Human CLASP-2

<400> 88

Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	Asn	Gln
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Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	Val	Asn
			20					25					30		
Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu	Gly
			35				40					45			
Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala	Glu
	50					55					60				
Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr	Lys
65					70					75					80
Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	Ser	Asn
				85					90						95
Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	Lys	Ser
			100					105					110		
Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn
	115						120					125			
Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn
	130					135					140				
Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala
145					150					155					160
Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe
			165						170					175	
Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile
			180					185					190		
Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe
	195						200					205			
Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn
	210					215					220				
Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu
225					230					235					240
Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu
				245					250					255	
Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg
			260					265					270		
Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys
	275						280					285			
His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile
	290					295					300				

Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln
 305 310 315 320
 Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met
 325 330 335
 Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val
 340 345 350
 Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu
 355 360 365
 Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro
 370 375 380
 Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser
 385 390 395 400
 Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn
 405 410 415
 Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val
 420 425 430
 Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys
 435 440 445
 Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr
 450 455 460
 Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
 465 470 475 480
 Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala
 485 490 495
 Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln
 500 505 510
 Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu
 515 520 525
 Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr
 530 535 540
 Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn
 545 550 555 560
 Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe
 565 570 575
 Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro
 580 585 590
 Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His
 595 600 605
 Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu
 610 615 620

Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys
 625 630 635 640
 Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser
 645 650 655
 Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn
 660 665 670
 Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln
 675 680 685
 Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly
 690 695 700
 Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn
 705 710 715 720
 Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp
 725 730 735
 Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys
 740 745 750
 Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu
 755 760 765
 Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp
 770 775 780
 Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala
 785 790 795 800
 Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg
 805 810 815
 Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro
 820 825 830
 Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp
 835 840 845
 Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala
 850 855 860
 Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr
 865 870 875 880
 Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp
 885 890 895
 Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu
 900 905 910
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly
 915 920 925
 Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys
 930 935 940
 Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro

945		950		955		960
Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg						
	965			970		975
Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr						
	980			985		990
Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile						
	995		1000		1005	
Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val						
	1010		1015		1020	
Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp						
	1025		1030		1035	1040
Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala						
		1045		1050		1055
Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser						
	1060		1065		1070	
Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp						
	1075		1080		1085	
Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys						
	1090		1095		1100	
Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val						
	1105		1110		1115	1120
Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met						
		1125		1130		1135
Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His						
	1140		1145		1150	
Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser						
	1155		1160		1165	
Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val						
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His Gly Met Thr Ser Ser Ser Val Val						
	1185		1190			

<210> 89

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Furin cleavage
consensus sequence

<400> 89

Arg Lys Gln Arg

1

<210> 90
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Human CLASP-2
predicted cleavage site by homology

<400> 90
Arg Asn Gln Arg
1

<210> 91
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
consensus motif E

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = any amino acid

<400> 91
Pro Glu Xaa Ala Ile Xaa Met
1 5

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
consensus motif F

<220>
<221> MOD_RES
<222> (1)..(15)
<223> Xaa is any amino acid.

<400> 92
Leu Xaa Met Xaa Leu Gly Xaa Val Xaa Xaa Xaa Val Asn Xaa Gly
1 5 10 15

<210> 93
<211> 125

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: CLASP-2C exon
 not found in CLASP-2A

 <220>
 <221> misc_feature
 <222> (1)..(125)
 <223> N is A, C, G, or T.

 <400> 93
 agggattttg agaggctggc ccatctgtat gacacgctgc accgggccta cagcaaagtg 60
 accgaggtca tgcactcggg ccgcagttnc tggggaccta cttccgggta gccttcttcg 120
 ggcag 125

 <210> 94
 <211> 44
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Amino acids
 encoded by CLASP-2C exon not found in CLASP-2A

 <400> 94
 Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala
 1 5 10 15
 Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly
 20 25 30
 Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
 35 40

 <210> 95
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer F1

 <400> 95
 cccagatttt tatgatgag 19

 <210> 96
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer R1

 <400> 96

gataatgaca aagttctgac 20

<210> 97
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer F2

<400> 97
ctggaaatct tgacaaaaat gc 22

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R2

<400> 98
gtctttttaa tacagatgtg g 21

<210> 99
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer F3

<400> 99
gagaggctgg cccatctgta tg 22

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
probe/primer R3

<400> 100
atcttcaaag aatccctgcc 20

<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
 probe/primer F4

<400> 101
 gaagcagtcc agtgggagcc g 21

<210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer R4

<400> 102
 gcctccccgg ctctcctca gg 22

<210> 103
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer R5

<400> 103
 cctccacatc tgtttcactg tc 22

<210> 104
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer F5

<400> 104
 ctccatgatg gaagacgtgg g 21

<210> 105
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer R6

<400> 105
 gatgagctcg tagcgctcgg c 21

<210> 106
 <211> 20

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer F6

 <400> 106
 cattggcgtt taagctcctg 20

 <210> 107
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer F7

 <400> 107
 ggacccatag ttcatgatcg 20

 <210> 108
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Exemplary
 probe/primer R4

 <400> 108
 cttcatcttc aagaaatccc tc 22

 <210> 109
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 1

 <400> 109
 gaaggcgatc atcacgtggc cttccatcgc 30

 <210> 110
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 2

 <400> 110
 gcttcaagta atgactgggtg cagaacatct g 31

<210> 111
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 3

 <400> 111
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 <210> 112
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 4

 <400> 112
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 <210> 113
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 5

 <400> 113
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 <210> 114
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Antisense
 oligo 6

 <400> 114
 caggagctgg ttcttaaa 18

 <210> 115
 <211> 81
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> Exon 1A

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 gtgaggatta ttacaattta a 81

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 <211> 118
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Exon 1B

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 aatcattgtt tagtcttcat ctttcacagc tcaggctgaa ggcctttcct tgctgaga 118

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 <211> 42
 <212> DNA
 <213> Homo sapiens

<220>
 <223> Exon 1C

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<210> 118
 <211> 6791
 <212> DNA
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<220>
 <221> CDS
 <222> (102)..(6044)

<220>
 <223> Human CLASP-2 gene

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 tccagaagaa gactcagatc ctgaacgact gtttacggga g atg ctg ctc ttc cct 116
 Met Leu Leu Phe Pro
 1 5

tac gat gac ttt cag acg gcc atc ctg aga cga cag ggt cga tac ata 164
 Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg Gln Gly Arg Tyr Ile
 10 15 20

tgc tca aca gtg cct gcg aag gcg gaa gag gaa gca cag agc ttg ttt 212
 Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Ala Gln Ser Leu Phe
 25 30 35

gtt aca gag tgc atc aaa acc tat aac tct gac tgg cat ctt gtg aac 260
 Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp Trp His Leu Val Asn
 40 45 50

tat	aaa	tat	gaa	gat	tac	tca	gga	gag	ttt	cga	cag	ctt	ccg	aac	aaa	308
Tyr	Lys	Tyr	Glu	Asp	Tyr	Ser	Gly	Glu	Phe	Arg	Gln	Leu	Pro	Asn	Lys	
	55					60					65					
gtg	gtc	aag	ttg	gat	aaa	ctt	cca	ggt	cat	gtc	tat	gaa	gtt	gac	gag	356
Val	Val	Lys	Leu	Asp	Lys	Leu	Pro	Val	His	Val	Tyr	Glu	Val	Asp	Glu	
	70				75					80					85	
gag	gtc	gac	aaa	gat	gag	gat	gct	gcc	tcc	ctt	ggt	tcc	cag	aag	ggt	404
Glu	Val	Asp	Lys	Asp	Glu	Asp	Ala	Ala	Ser	Leu	Gly	Ser	Gln	Lys	Gly	
				90					95					100		
ggg	atc	acc	aag	cat	ggc	tgg	ctg	tac	aaa	ggc	aac	atg	aac	agt	gcc	452
Gly	Ile	Thr	Lys	His	Gly	Trp	Leu	Tyr	Lys	Gly	Asn	Met	Asn	Ser	Ala	
			105					110					115			
atc	agc	gtg	acc	atg	agg	tca	ttt	aag	aga	cga	ttt	ttc	cac	ctg	att	500
Ile	Ser	Val	Thr	Met	Arg	Ser	Phe	Lys	Arg	Arg	Phe	Phe	His	Leu	Ile	
		120					125					130				
caa	ctt	ggc	gat	gga	tcc	tat	aat	ttg	aat	ttt	tat	aaa	gat	gaa	aag	548
Gln	Leu	Gly	Asp	Gly	Ser	Tyr	Asn	Leu	Asn	Phe	Tyr	Lys	Asp	Glu	Lys	
	135					140					145					
atc	tcc	aaa	gaa	cca	aaa	gga	tca	ata	ttt	ctg	gat	tcc	tgt	atg	ggt	596
Ile	Ser	Lys	Glu	Pro	Lys	Gly	Ser	Ile	Phe	Leu	Asp	Ser	Cys	Met	Gly	
	150				155					160					165	
gtc	gtt	cag	aac	aac	aaa	gtc	agg	cgt	ttt	gct	ttt	gag	ctc	aag	atg	644
Val	Val	Gln	Asn	Asn	Lys	Val	Arg	Arg	Phe	Ala	Phe	Glu	Leu	Lys	Met	
				170					175					180		
cag	gac	aaa	agt	agt	tat	ctc	ttg	gca	gca	gac	agt	gaa	gtg	gaa	atg	692
Gln	Asp	Lys	Ser	Ser	Tyr	Leu	Leu	Ala	Ala	Asp	Ser	Glu	Val	Glu	Met	
			185					190					195			
gaa	gaa	tgg	atc	aca	att	cta	aat	aag	atc	ctc	cag	ctc	aac	ttt	gaa	740
Glu	Glu	Trp	Ile	Thr	Ile	Leu	Asn	Lys	Ile	Leu	Gln	Leu	Asn	Phe	Glu	
		200					205					210				
gct	gca	atg	caa	gaa	aag	cga	aat	ggc	gac	tct	cac	gaa	gat	gat	gaa	788
Ala	Ala	Met	Gln	Glu	Lys	Arg	Asn	Gly	Asp	Ser	His	Glu	Asp	Asp	Glu	
	215					220					225					
caa	agc	aaa	ttg	gaa	ggt	tct	ggt	tcc	ggt	tta	gat	agc	tac	ctg	ccg	836
Gln	Ser	Lys	Leu	Glu	Gly	Ser	Gly	Ser	Gly	Leu	Asp	Ser	Tyr	Leu	Pro	
	230				235					240					245	
gaa	ctt	gcc	aag	agt	gca	aga	gaa	gca	gaa	atc	aaa	cta	aaa	agt	gaa	884
Glu	Leu	Ala	Lys	Ser	Ala	Arg	Glu	Ala	Glu	Ile	Lys	Leu	Lys	Ser	Glu	
				250					255					260		
agc	aga	gtc	aaa	ctt	ttt	tat	ttg	gac	cca	gat	gcc	cag	aag	ctt	gac	932
Ser	Arg	Val	Lys	Leu	Phe	Tyr	Leu	Asp	Pro	Asp	Ala	Gln	Lys	Leu	Asp	
			265					270					275			
ttc	tca	tca	gct	gag	cca	gaa	gtg	aag	tca	ttt	gaa	gag	aag	ttt	gga	980
Phe	Ser	Ser	Ala	Glu	Pro	Glu	Val	Lys	Ser	Phe	Glu	Glu	Lys	Phe	Gly	
		280					285						290			

aaa agg atc ctt gtc aag tgc aat gat tta tct ttc aat ttg caa tgc	1028
Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser Phe Asn Leu Gln Cys	
295 300 305	
tgt gtt gcc gaa aat gaa gaa gga ccc act aca aat gtt gaa cct ttc	1076
Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr Asn Val Glu Pro Phe	
310 315 320 325	
ttt gtt act cta tcc ctg ttt gac ata aaa tac aac cgg aag att tct	1124
Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr Asn Arg Lys Ile Ser	
330 335 340	
gcc gat ttc cac gta gac ctg aac cat ttc tca gtg agg caa atg ctc	1172
Ala Asp Phe His Val Asp Leu Asn His Phe Ser Val Arg Gln Met Leu	
345 350 355	
gcc acc acg tcc ccg gcg ctg atg aat ggc agt ggg cag agc cca tct	1220
Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser Gly Gln Ser Pro Ser	
360 365 370	
gtc ctc aag ggc atc ctt cat gaa gcc gcc atg cag tat ccg aag cag	1268
Val Leu Lys Gly Ile Leu His Glu Ala Ala Met Gln Tyr Pro Lys Gln	
375 380 385	
gga ata ttt tca gtc act tgt cct cat cca gat ata ttt ctt gtg gcc	1316
Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp Ile Phe Leu Val Ala	
390 395 400 405	
aga att gaa aaa gtc ctt cag ggg agc atc aca cat tgc gct gag cca	1364
Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr His Cys Ala Glu Pro	
410 415 420	
tat atg aaa agt tca gac tct tct aag gtg gcc cag aag gtg ctg aag	1412
Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala Gln Lys Val Leu Lys	
425 430 435	
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Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln Tyr Arg Met Pro Phe	
440 445 450	
gct tgg gca gca agg aca ttg ttt aag gat gca tct gga aat ctt gac	1508
Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala Ser Gly Asn Leu Asp	
455 460 465	
aaa aat gcc aga ttt tct gcc atc tac agg caa gac agc aat aag cta	1556
Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln Asp Ser Asn Lys Leu	
470 475 480 485	
tcc aat gat gac atg ctc aag tta ctt gca gac ttt cgg aaa cct gag	1604
Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp Phe Arg Lys Pro Glu	
490 495 500	
aag atg gct aag ctc cca gtg att tta ggc aat cta gac att aca att	1652
Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn Leu Asp Ile Thr Ile	
505 510 515	
gat aat gtt tcc tca gac ttc cct aat tat gtt aat tca tca tac att	1700
Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val Asn Ser Ser Tyr Ile	
520 525 530	
ccc aca aaa caa ttt gaa acc tgc agt aaa act ccc atc acg ttt gaa	1748

Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	Pro	Ile	Thr	Phe	Glu		
535						540					545						
gtg	gag	gaa	ttt	gtg	ccc	tgc	ata	cca	aaa	cac	act	cag	cct	tac	acc	1796	
Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His	Thr	Gln	Pro	Tyr	Thr		
550					555					560					565		
atc	tac	acc	aat	cac	ctt	tac	gtt	tat	cct	aag	tac	ttg	aaa	tac	gac	1844	
Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	Tyr	Leu	Lys	Tyr	Asp		
				570					575					580			
agt	cag	aag	tct	ttt	gcc	aag	gct	aga	aat	att	gcg	att	tgc	att	gaa	1892	
Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Ile	Cys	Ile	Glu		
			585					590					595				
ttc	aaa	gat	tca	gat	gag	gaa	gac	tct	cag	ccc	ctt	aag	tgc	att	tat	1940	
Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	Leu	Lys	Cys	Ile	Tyr		
		600					605					610					
ggc	aga	cct	ggt	ggg	cca	gtt	ttc	aca	aga	agc	gcc	ttt	gct	gca	gtt	1988	
Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	Ala	Phe	Ala	Ala	Val		
		615				620					625						
tta	cac	cat	cac	caa	aac	cca	gaa	ttt	tat	gat	gag	att	aaa	ata	gag	2036	
Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu		
630					635					640					645		
ttg	ccc	act	cag	ctg	cat	gaa	aag	cac	cac	ctg	ttg	ctc	aca	ttc	ttc	2084	
Leu	Pro	Thr	Gln	His	Glu	Lys	His	His	Leu	Leu	Leu	Leu	Thr	Phe	Phe		
				650				655						660			
cat	gtc	agc	tgt	gac	aac	tca	agt	aaa	gga	agc	acg	aag	aag	agg	gat	2132	
His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	Asp		
			665					670					675				
gtc	gtt	gaa	acc	caa	gtt	ggc	tac	tcc	tgg	ctt	ccc	ctc	ctg	aaa	gac	2180	
Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	Asp		
		680					685					690					
gga	agg	gtg	gtg	aca	agc	gag	cag	cac	atc	ccg	gtc	tcg	gcg	tac	ctt	2228	
Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Tyr	Leu		
		695				700					705						
cct	tcg	ggc	cat	ctt	ggc	tac	caa	gag	ctt	ggg	atg	ggc	agg	cat	tat	2276	
Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	Tyr		
710					715					720					725		
ggc	ccg	gaa	att	aaa	tgg	gta	gat	gga	ggc	aag	cca	ctg	ctg	aaa	att	2324	
Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	Ile		
				730				735						740			
tcc	act	cat	ctg	gtt	tct	aca	gtg	tat	act	cag	gat	cag	cat	tta	cat	2372	
Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	His		
				745				750					755				
aat	ttt	ttc	cag	tac	tgt	cag	aaa	acc	gaa	tct	gga	gcc	caa	gcc	tta	2420	
Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	Leu		
		760					765					770					
gga	aac	gaa	ctt	gta	aag	tac	ctt	aag	agt	ctg	cat	gcg	atg	gaa	ggc	2468	
Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	Gly		

775	780	785	
cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc cga			2516
His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg			
790	795	800	805
gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act cgg			2564
Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr Arg			
	810	815	820
gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag agc			2612
Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu Ser			
	825	830	835
cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat gtt			2660
His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val			
	840	845	850
gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg acc			2708
Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met Thr			
	855	860	865
acg att ctc aag cct tct gcc gat ttc ctc acc agc aac aaa cta ctg			2756
Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu			
	870	875	880
agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct cag			2804
Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala Gln			
	890	895	900
cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga aac cag aga ttt			2852
His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg Phe			
	905	910	915
cct gca tcc tat cat cat gca gcg gaa acc gtt gta aat atg ctg atg			2900
Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu Met			
	920	925	930
cca cac atc act cag aag ttt gga gat aat cca gag gca tct aag aac			2948
Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn			
	935	940	945
gcg aat cat agc ctt gct gtc ttc atc aag aga tgt ttc acc ttc atg			2996
Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe Met			
	950	955	960
gac agg ggc ttt gtc ttc aag cag atc aac aac tac att agc tgt ttt			3044
Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe			
	970	975	980
gct cct gga gac cca aag acc ctc ttt gaa tac aag ttt gaa ttt ctc			3092
Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu			
	985	990	995
cgt gta gtg tgc aac cat gaa cat tat att ccg ttg aac tta cca atg			3140
Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met			
	1000	1005	1010
cca ttt gga aaa ggc agg att caa aga tac caa gac ctc cag ctt gac			3188
Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp			
	1015	1020	1025

tac tca tta aca gat gag ttc tgc aga aac cac ttc ttg gtg gga ctg Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly Leu 1030 1035 1040 1045	3236
tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc cgg gag gtc cgt Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val Arg 1050 1055 1060	3284
ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata aag cat tct ttt Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser Phe 1065 1070 1075	3332
gat gac aga tat gct tca agg agc cat cag gca agg ata gcc acc ctc Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr Leu 1080 1085 1090	3380
tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc cag cgg atc aat Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile Asn 1095 1100 1105	3428
gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc atg acc gtg aag Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val Lys 1110 1115 1120 1125	3476
gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg gtg acg ccg cag Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro Gln 1130 1135 1140	3524
aag gga agc acc ctg gac aac agc ctg cac aag gac ctg ctg ggc gcc Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly Ala 1145 1150 1155	3572
atc tcc ggc att gct tct cca tat aca acc tca act cca aac atc aac Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn 1160 1165 1170	3620
agt gtg aga aat gct gat tcg aga gga tct ctc ata agc aca gat tcg Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser 1175 1180 1185	3668
ggt aac agc ctt cca gaa agg aat agt gag aag agc aat tcc ctg gat Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp 1190 1195 1200 1205	3716
aag cac caa caa agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp 1210 1215 1220	3764
aaa ctt gac cag tct gag att aag agc cta ctg atg tgt ttc ctc tac Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr 1225 1230 1235	3812
atc tta aag agc atg tct gat gat gct ttg ttt aca tat tgg aac aag Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys 1240 1245 1250	3860
gct tca aca tct gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys 1255 1260 1265	3908

ctg cac cag ttc cag tac atg ggg aag cga tac ata gcc agg aac cag Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln 1270 1275 1280 1285	3956
gag ggg ttg gga ccc ata gtt cat gat cga aag tct cag aca ttg cct Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu Pro 1290 1295 1300	4004
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ggc agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac tcg Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser 1320 1325 1330	4100
gac gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct act Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr 1335 1340 1345	4148
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aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct gaa Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu 1385 1390 1395	4292
acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat aag Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys 1400 1405 1410	4340
ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct ctg Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu 1415 1420 1425	4388
tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc agg Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg 1430 1435 1440 1445	4436
acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt gat Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp 1450 1455 1460	4484
tac act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc ata Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile 1465 1470 1475	4532
tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc aga Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr Arg 1480 1485 1490	4580
ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac cgg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg 1495 1500 1505	4628
ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc aaa	4676

1750	1755	1760	1765	
atc cgc cgc ttc atg ttt gag atg cca ttt acg cag acc ggg aag agg				5444
Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg				
1770		1775	1780	
cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca gcc				5492
Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala				
1785	1790		1795	
ata cac tgc ttc cct tat gtg aag aag cgc atc cct gtc atg tac cag				5540
Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln				
1800	1805		1810	
cac cac act gac ctg aac ccc atc gag gtg gcc att gac gag atg agt				5588
His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser				
1815	1820		1825	
aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg gac				5636
Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp				
1830	1835	1840	1845	
atg atc aaa ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag gtc				5684
Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val				
1850	1855		1860	
aat gct ggc cca cta gca tat gcg cga gct ttc tta gat gat aca aac				5732
Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn				
1865	1870		1875	
aca aag cga tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt ttc				5780
Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe				
1880	1885		1890	
agg caa ttt gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa cgt				5828
Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg				
1895	1900		1905	
ctg att aaa gaa gac cag ctc gag tat cag gaa gaa atg aaa gcc aac				5876
Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn				
1910	1915	1920	1925	
tac agg gaa atg gcg aag gag ctt tct gaa atc atg cat gag cag atc				5924
Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile				
1930	1935		1940	
tgc ccc ctg gag gag aag acg agc gtc tta ccg aat tcc ctt cac atc				5972
Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile				
1945	1950		1955	
ttc aac gcc atc agt ggg act cca aca agc aca atg gtt cac ggg atg				6020
Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met				
1960	1965		1970	
acc agc tcg tct tcg gtc gtg tga ttacatctca tggcccgtgt gtggggactt				6074
Thr Ser Ser Ser Ser Val Val				
1975	1980			
gctttgtcat ttgcaaactc aggatgcttt ccaaagccaa tcaactgggga gaccgagcac				6134
agggaggacc aaggggaagg ggagagaaag gaaataaaga acaacgttat ttcttaacag				6194

actttctata ggagttgtaa gaaggtgcac atatTTTTTT aaatctcact ggcaatatTC 6254
aaagttttca ttgtgtctta acaaaggtgt ggtagacact cttgagctgg acttagattt 6314
tattcttcct tgcagagtag tgttagaata gatggcctac agaaaaaaaa ggttctggga 6374
tctacatggc agggagggct gcaactgacat tgatgcctgg gggacctttt gcctcgactc 6434
gtgccggaaa tctgatcgta atcagggtag agaacttact agttttgtct aggagtatgt 6494
tgtatgacta ggatttgtgc tattatctca ttcaacaaca tagagcaaga atagttagct 6554
aactgagcta gacactcaat taatccgcta ctggcttcaa gtcagaactt tgtcattaat 6614
catcgactcc gggacggta tatatgtatt acatttctac atttttaata ctcacatggg 6674
cttatgcatt aagtttaatt gtgataaatt tgtgctggc cagtatatgc aatacacttt 6734
aatggtttat tcttgtcata aaaatgtgca atatggagat gtatacaagt ctttact 6791

<210> 119
<211> 1980
<212> PRT
<213> Homo sapiens
<223> Human CLASP-2 gene

<400> 119
Met Leu Leu Phe Pro Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg
1 5 10 15
Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
20 25 30
Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
35 40 45
Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
50 55 60
Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
65 70 75 80
Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
85 90 95
Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
100 105 110
Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
115 120 125
Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
130 135 140
Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
145 150 155 160
Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
165 170 175
Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
180 185 190
Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
195 200 205
Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
210 215 220
His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
225 230 235 240
Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
245 250 255

Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
 260 265 270
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
 275 280 285
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
 290 295 300
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr
 305 310 315 320
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
 325 330 335
 Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
 340 345 350
 Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
 355 360 365
 Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
 370 375 380
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
 385 390 395 400
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
 405 410 415
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
 420 425 430
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
 435 440 445
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
 450 455 460
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
 465 470 475 480
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
 485 490 495
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
 500 505 510
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
 515 520 525
 Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr
 530 535 540
 Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His
 545 550 555 560
 Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys
 565 570 575
 Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile
 580 585 590
 Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro
 595 600 605
 Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser
 610 615 620
 Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp
 625 630 635 640
 Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu
 645 650 655
 Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser
 660 665 670
 Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu
 675 680 685
 Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro
 690 695 700
 Val Ser Ala Tyr Leu Pro Ser Gly His Leu Gly Tyr Gln Glu Leu Gly
 705 710 715 720
 Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys
 725 730 735
 Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln

740					745					750					
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser
755					760					765					
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu
770					775					780					
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu
785					790					795					
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala
805					810					815					
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu
820					825					830					
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys
835					840					845					
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu
850					855					860					
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr
865					870					875					
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile
885					890					895					
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu
900					905					910					
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val
915					920					925					
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro
930					935					940					
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg
945					950					955					
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn
965					970					975					
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr
980					985					990					
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro
995					1000					1005					
Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln
1010					1015					1020					
Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His
1025					1030					1035					
Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu
1045					1050					1055					
Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu
1060					1065					1070					
Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala
1075					1080					1085					
Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn
1090					1095					1100					
Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala
1105					1110					1115					
Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro
1125					1130					1135					
Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys
1140					1145					1150					
Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser
1155					1160					1165					
Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu
1170					1175					1180					
Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys
1185					1190					1195					
Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser
1205					1210					1215					
Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu
1220					1225					1230					

Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
 Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
 Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
 1475 1480 1485
 Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
 1490 1495 1500
 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1525 1530 1535
 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550
 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 1635 1640 1645
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660
 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680
 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn

1715 1720 1725
 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740
 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760
 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805
 Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
 1940 1945 1950
 Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
 1955 1960 1965
 Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
 1970 1975 1980

<210> 120
 <211> 179
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CLASP-2 exon 1

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 gaaaatgtca tcgtccagaa gaagactcag atcctgaacg actgtttacg ggagatgctg 120
 ctcttccctt acgatgactt tcaggtaagt aacgttatgt ttctatccgt agaaccacg 179

<210> 121
 <211> 183
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CLASP-2 exon 2

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cagaggtaag gctctttcct gcattaatth acattttgaa gtcattttcc cctaactgcc 180
tcc 183

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<211> 151
<212> DNA
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<220>
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agctatatta tacacatagg gaaaagtctt t 151

<210> 123
<211> 147
<212> DNA
<213> Homo sapiens

<220>
<223> CLASP-2 exon 4

<400> 123
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ttcatgtcta tgaagttgac gaggaggtcg acaaagatga ggtgggatac ctgcttgctg 120
ttgcttctct tttcactcta gatttaa 147

<210> 124
<211> 176
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 5

<400> 124
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aggggtgggat caccaagcat ggctggctgt acaaaggcaa catgaacagt gccatcagcg 120
tgaccatgag ggtgaggacg cacatcactt tgccctcccc tctcacaagc cctttc 176

<210> 125
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 6

<400> 125
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gattcaactt ggcgatggat cctataatth gaatttttat aaagatgaaa agatctccaa 120
agaacaaaa ggatcaatat ttctggattc ctgtatgggt gtcgttcagg taaatatgaa 180
aagagtttta ccattatggt ttctta 206

<210> 126
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 7

<400> 126
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agctcaagat gcaggacaaa agtagttatc tcttggcagc agacagtga gtggaaatgg 120
aagaatggat cacaattcta aataagatcc tccagctcaa ctttgaagct gcaatgcaag 180
aaaagcgaaa tggcgactct cacgaaggta gataggcttg gcttcccca ggcacataca 240
cactct 246

<210> 127
<211> 144
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 8

<400> 127
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aggttctggg tccggttttag atagctacct gccggaactt gccaaagtaa catcgtctta 120
tatcttctgc tcttcgttga atgc 144

<210> 128
<211> 152
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 9

<400> 128
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actatctaaa tgtttaatat ttaaaaccaa at 152

<210> 129
<211> 222
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 10

<400> 129
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atttttcatt ttaaaaataa acattaaaaa aaaaataggc ag 222

<210> 130
<211> 289

<212> DNA
<213> Homo sapiens

<220>
<223> Exon 11

<400> 130
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atttctcagt gaggcaaagt ctgccacca cgtccccggc gctgatgaat ggcagtgggc 180
agagcccatac tgcctcaag ggcattcttc atgaagccgc catgcagtat ccgaagcagg 240
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<211> 205
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 12

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ttgcgctgag ccatatatga aaagttcaga ctcttctaag gtatgaatgg cttttacgct 180
ttggggtggt aaaaagcaat ctgaa 205

<210> 132
<211> 166
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 13

<400> 132
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aggaacacct tttatacctt ttaaatacgat atagataggt gcatgg 166

<210> 133
<211> 159
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 14

<400> 133
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caatgatgac atgctcaagt tacttgacaga ctttcggaa 159

<210> 134
<211> 43545
<212> DNA
<213> Homo sapiens

<220>

<223> Genomic DNA at the CLASP-2 locus.

<400> 134

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tgaacaagca tcaactctgt tagcaggaca ccaccagca ttttttgtcc ctttggaac 180
aactcttatt tctgtttctt tgtgatacca aaactagcat actctaattg tagaaaatac 240
aaaacataga gtagaacata ctaagttctt tatcttaaga aatggcattt gtgtatgaga 300
atgtcttgct tatcttttct ccctccaggc aaagccaaag ctaattgagc cactcgacta 360
tgaaaaatgt atcgtccaga agaagactca gatcctgaac gactgtttac gggagatgct 420
gctcttcctt tacgatgact ttcaggtaag taacgttatg tttctatccg tagaaccacg 480
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Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser 1715	1720	1725
Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr 1730	1735	1740
Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu 1745	1750	1755 1760
Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr 1765	1770	1775
Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn 1780	1785	1790
His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly 1795	1800	1805
Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu 1810	1815	1820
Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn 1825	1830	1835 1840
Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu 1845	1850	1855
Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp 1860	1865	1870
Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val 1875	1880	1885
Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp 1890	1895	1900

Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
 1985 1990 1995 2000
 Gly Ser Pro Arg Tyr Ala Glu Val
 2005

<210> 136
 <211> 2015
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CLASP-5 amino acid sequence

<400> 136
 Met Thr His Leu Asn Ser Leu Asp Val Gln Leu Ala Gln Glu Leu Gly
 1 5 10 15
 Asp Phe Thr Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys
 20 25 30
 Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro
 35 40 45
 His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
 50 55 60
 Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr
 65 70 75 80
 Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
 85 90 95
 Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
 100 105 110
 His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
 115 120 125
 Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
 130 135 140
 Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu
 145 150 155 160

Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser
 165 170 175
 Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro
 180 185 190
 Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
 195 200 205
 Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
 210 215 220
 Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
 225 230 235 240
 Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
 245 250 255
 Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
 260 265 270
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
 275 280 285
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
 290 295 300
 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
 305 310 315 320
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
 325 330 335
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
 340 345 350
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg
 355 360 365
 Arg Thr Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu
 370 375 380
 Glu Glu Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val
 385 390 395 400
 Ser Ser Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu
 405 410 415
 Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
 420 425 430
 Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
 435 440 445
 Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro
 450 455 460
 Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
 465 470 475 480

Thr Arg Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr
 485 490 495
 Val Tyr Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg
 500 505 510
 Asn Ile Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn
 515 520 525
 Ala Met Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln
 530 535 540
 Glu Val Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr
 545 550 555 560
 Glu Glu Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His
 565 570 575
 Leu Leu Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala
 580 585 590
 Ser Val Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn
 595 600 605
 Glu Arg Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys
 610 615 620
 Leu Pro Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln
 625 630 635 640
 Asn Pro Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile
 645 650 655
 Glu Val Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu
 660 665 670
 Lys Phe Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro
 675 680 685
 Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu
 690 695 700
 Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu
 705 710 715 720
 Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val
 725 730 735
 Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala
 740 745 750
 Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp
 755 760 765
 Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val
 770 775 780
 His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser
 785 790 795 800
 Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly

Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215
 Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
 1330 1335 1340
 Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
 1345 1350 1355 1360
 Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
 1365 1370 1375
 Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
 1380 1385 1390
 Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
 1395 1400 1405
 Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
 1410 1415 1420
 His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
 1425 1430 1435 1440
 Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
 1445 1450 1455

Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
 1460 1465 1470
 Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
 1475 1480 1485
 Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
 1490 1495 1500
 Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
 1505 1510 1515 1520
 Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
 1525 1530 1535
 Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660
 Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu

1780	1785	1790
Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg 1795 1800 1805		
Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu 1810 1815 1820		
Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala 1825 1830 1835 1840		
Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe 1845 1850 1855		
Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr 1860 1865 1870		
Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met 1875 1880 1885		
Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly 1890 1895 1900		
Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro 1905 1910 1915 1920		
Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe 1925 1930 1935		
Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr 1940 1945 1950		
Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys 1955 1960 1965		
Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu 1970 1975 1980		
Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His 1985 1990 1995 2000		
Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser 2005 2010 2015		

<210> 137

<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> CLASP-3 amino acid sequence

<400> 137

Met	Ala	Glu	Arg	Arg	Ala	Phe	Ala	Gln	Lys	Ile	Ser	Arg	Thr	Val	Ala
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Ala	Glu	Val	Arg	Lys	Gln	Ile	Ser	Gly	Gln	Tyr	Ser	Gly	Ser	Pro	Gln
		20						25					30		

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr

35					40					45						
Val	Pro	Leu	Thr	Glu	Ala	Val	Asp	Pro	Val	Asp	Leu	Glu	Asp	Tyr	Leu	
50					55					60						
Ile	Thr	His	Pro	Leu	Ala	Val	Asp	Ser	Gly	Pro	Leu	Arg	Asp	Leu	Ile	
65					70					75					80	
Glu	Phe	Pro	Pro	Asp	Asp	Ile	Glu	Val	Val	Tyr	Ser	Pro	Arg	Asp	Cys	
					85					90					95	
Arg	Thr	Leu	Val	Ser	Ala	Val	Pro	Glu	Glu	Ser	Glu	Met	Asp	Pro	His	
					100					105					110	
Val	Arg	Asp	Cys	Ile	Arg	Ser	Tyr	Thr	Glu	Asp	Trp	Ala	Ile	Val	Ile	
					115					120					125	
Arg	Lys	Tyr	His	Lys	Leu	Gly	Thr	Gly	Phe	Asn	Pro	Asn	Thr	Leu	Asp	
					130					135					140	
Lys	Gln	Lys	Glu	Arg	Gln	Lys	Gly	Leu	Pro	Lys	Gln	Val	Phe	Glu	Ser	
145					150					155					160	
Asp	Glu	Ala	Pro	Asp	Gly	Asn	Ser	Tyr	Gln	Asp	Asp	Gln	Asp	Asp	Leu	
					165					170					175	
Lys	Arg	Arg	Ser	Met	Ser	Ile	Asp	Asp	Thr	Pro	Arg	Gly	Ser	Trp	Ala	
					180					185					190	
Cys	Ser	Ile	Phe	Asp	Leu	Lys	Asn	Ser	Leu	Pro	Asp	Ala	Leu	Leu	Pro	
195					200					205						
Asn	Leu	Leu	Asp	Arg	Thr	Pro	Asn	Glu	Glu	Ile	Asp	Arg	Gln	Asn	Asp	
210					215					220						
Asp	Gln	Arg	Lys	Ser	Asn	Arg	His	Lys	Glu	Leu	Phe	Ala	Leu	His	Pro	
225					230					235					240	
Ser	Pro	Asp	Glu	Glu	Glu	Pro	Ile	Glu	Arg	Leu	Ser	Val	Pro	Asp	Ile	
					245					250					255	
Pro	Lys	Glu	His	Phe	Gly	Gln	Arg	Leu	Leu	Val	Lys	Cys	Leu	Ser	Leu	
					260					265					270	
Lys	Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	Ala	Ser	Leu	Ala	Leu	Tyr	
275					280					285						
Asp	Val	Lys	Glu	Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	
290					295					300						
Asn	Ser	Glu	Gln	Met	Lys	Gly	Leu	Leu	Arg	Pro	His	Val	Pro	Pro	Ala	
305					310					315					320	
Ala	Ile	Thr	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Ile	Thr	Tyr	Pro	
					325					330					335	
Ser	Gln	Asp	Val	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	
					340					345					350	
Gly	Asp	Ile	Gly	Glu	Cys	Ala	Glu	Pro	Tyr	Met	Ile	Phe	Lys	Glu	Ala	
355					360					365						

Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430
 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560
 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
 565 570 575
 Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
 580 585 590
 Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
 595 600 605
 Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
 610 615 620
 Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
 625 630 635 640
 Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
 645 650 655
 Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
 660 665 670
 Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
 675 680 685

Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
690 695 700
Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
705 710 715 720
Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
725 730 735
Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
740 745 750
Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
755 760 765
Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
770 775 780
Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
785 790 795 800
Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
805 810 815
Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
820 825 830
Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
835 840 845
Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
850 855 860
Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
865 870 875 880
Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
885 890 895
Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
900 905 910
Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
915 920 925
Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
930 935 940
Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
945 950 955 960
Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
965 970 975
Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
980 985 990
Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
995 1000 1005
Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr

Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660

Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710
 Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala

1985	1990	1995	2000
Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln	2005	2010	2015
Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln	2020	2025	2030
Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His	2035	2040	2045
Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp	2050	2055	2060
Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr	2065	2070	2080
Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro	2085	2090	

<210> 138

<211> 2047

<212> PRT

<213> Homo sapiens

<220>

<223> CLASP-7 amino acid sequence

<400> 138

Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr	1	5	10	15
Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser	20	25	30	
Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr	35	40	45	
Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro	50	55	60	
Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala	65	70	75	80
Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu	85	90	95	
Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala	100	105	110	
Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln	115	120	125	
Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu	130	135	140	
Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly	145	150	155	160
Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser				

Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605
 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735
 Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
 805 810 815

Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860
 Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940
 His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960
 Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975
 Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990
 Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
 1010 1015 1020
 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055
 Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys Lys Ala Ile
 1125 1130 1135
 Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp Pro Arg Tyr

1140	1145	1150
Ala Glu Ala Thr Val Lys Ala Arg Val Ala Glu Leu Tyr Leu Pro Leu		
1155	1160	1165
Leu Ser Ile Ala Arg Asp Thr Leu Pro Arg Leu His Asp Phe Ala Glu		
1170	1175	1180
Gly Pro Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr		
1185	1190	1195
Glu Gly Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met		
1205	1210	1215
Ala Ile Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser		
1220	1225	1230
Gln Gly Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu		
1235	1240	1245
Ser Ser Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr		
1250	1255	1260
Glu Pro Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln		
1265	1270	1275
Leu Gly Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu		
1285	1290	1295
Tyr Lys Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys		
1300	1305	1310
Lys Ser Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr		
1315	1320	1325
Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro		
1330	1335	1340
Phe Gly Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp		
1345	1350	1355
Lys Gln Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His		
1365	1370	1375
Glu Ala Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val		
1380	1385	1390
Leu Asp Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala		
1395	1400	1405
Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu		
1410	1415	1420
Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln		
1425	1430	1435
Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr		
1445	1450	1455
Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser		
1460	1465	1470

Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu
 1475 1480 1485
 Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met
 1490 1495 1500
 Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe
 1505 1510 1515 1520
 Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala
 1525 1530 1535
 Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln
 1540 1545 1550
 Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met
 1555 1560 1565
 Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg
 1570 1575 1580
 Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu
 1585 1590 1595 1600
 Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala
 1605 1610 1615
 Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala
 1620 1625 1630
 Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln
 1635 1640 1645
 Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile
 1650 1655 1660
 Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu
 1665 1670 1675 1680
 Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met
 1685 1690 1695
 Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro
 1700 1705 1710
 Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly
 1715 1720 1725
 Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp
 1730 1735 1740
 Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His
 1745 1750 1755 1760
 Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile
 1765 1770 1775
 Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu
 1780 1785 1790

Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val
 1795 1800 1805
 Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr
 1810 1815 1820
 Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr
 1825 1830 1835 1840
 Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe
 1845 1850 1855
 Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg
 1860 1865 1870
 Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg
 1875 1880 1885
 Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val
 1890 1895 1900
 Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr
 1905 1910 1915 1920
 Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly
 1925 1930 1935
 Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val
 1940 1945 1950
 Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn
 1955 1960 1965
 Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala
 1970 1975 1980
 Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His
 1985 1990 1995 2000
 Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro
 2005 2010 2015
 Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly
 2020 2025 2030
 Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
 2035 2040 2045

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 <211> 2180
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> CLASP-1 amino acid sequence

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 1 5 10 15

Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg
 20 25 30
 Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu
 35 40 45
 Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
 50 55 60
 Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
 65 70 75 80
 Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
 85 90 95
 Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
 100 105 110
 Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
 115 120 125
 Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
 130 135 140
 Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
 145 150 155 160
 Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val
 165 170 175
 Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
 180 185 190
 Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
 195 200 205
 Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
 210 215 220
 Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
 225 230 235 240
 Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met
 245 250 255
 Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met
 260 265 270
 Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu
 275 280 285
 Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu
 290 295 300
 Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr
 305 310 315 320
 Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr
 325 330 335
 Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn

340				345				350								
Leu	Phe	Ser	Leu	Asp	Pro	Asp	Ile	Asp	Thr	Leu	Lys	Leu	Gln	Lys	Lys	
		355					360					365				
Asp	Leu	Leu	Glu	Pro	Glu	Ser	Val	Ile	Lys	Pro	Phe	Glu	Glu	Lys	Ala	
		370					375					380				
Ala	Lys	Arg	Ile	Met	Ile	Ile	Cys	Lys	Ala	Leu	Asn	Ser	Asn	Leu	Gln	
385					390					395						400
Gly	Cys	Val	Thr	Glu	Asn	Glu	Asn	Asp	Pro	Ile	Thr	Asn	Ile	Glu	Pro	
				405					410					415		
Phe	Phe	Val	Ser	Val	Ala	Leu	Tyr	Asp	Leu	Arg	Asp	Ser	Arg	Lys	Ile	
				420					425					430		
Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met	
		435					440					445				
Leu	Leu	Gly	Ala	Ser	Val	Ala	Leu	Glu	Asn	Gly	Asn	Ile	Asp	Thr	Ile	
		450					455					460				
Thr	Pro	Arg	Gln	Ser	Glu	Glu	Pro	His	Ile	Lys	Gly	Leu	Pro	Glu	Glu	
465					470					475						480
Trp	Leu	Lys	Phe	Pro	Lys	Gln	Ala	Val	Phe	Ser	Val	Ser	Asn	Pro	His	
				485					490					495		
Ser	Glu	Ile	Val	Leu	Val	Ala	Lys	Ile	Glu	Lys	Val	Leu	Met	Gly	Asn	
				500					505					510		
Ile	Ala	Ser	Gly	Ala	Glu	Pro	Tyr	Ile	Lys	Asn	Pro	Asp	Ser	Asn	Lys	
		515					520					525				
Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu	
		530					535					540				
Gly	Lys	Tyr	Arg	Arg	Ala	Phe	Ala	Trp	Ala	Val	Arg	Ser	Val	Phe	Lys	
545					550					555						560
Asp	Asn	Gln	Gly	Asn	Val	Asp	Arg	Asp	Ser	Arg	Phe	Ser	Pro	Leu	Phe	
				565					570					575		
Arg	Gln	Glu	Ser	Ser	Lys	Ile	Ser	Thr	Glu	Asp	Leu	Val	Lys	Leu	Val	
				580					585					590		
Ser	Asp	Tyr	Arg	Arg	Ala	Asp	Arg	Ile	Ser	Lys	Met	Gln	Thr	Ile	Pro	
		595					600					605				
Gly	Ser	Leu	Asp	Ile	Ala	Val	Asp	Asn	Val	Pro	Leu	Glu	His	Pro	Asn	
		610					615					620				
Cys	Val	Thr	Ser	Ser	Phe	Ile	Pro	Val	Lys	Pro	Phe	Asn	Met	Met	Ala	
625					630					635						640
Gln	Thr	Glu	Pro	Thr	Val	Glu	Val	Glu	Glu	Phe	Val	Tyr	Asp	Ser	Thr	
				645					650					655		
Lys	Tyr	Cys	Arg	Pro	Tyr	Arg	Val	Tyr	Lys	Asn	Gln	Ile	Tyr	Ile	Tyr	
				660					665					670		

Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
 675 680 685
 Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
 690 695 700
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
 705 710 715 720
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
 725 730 735
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
 740 745 750
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
 755 760 765
 Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
 770 775 780
 Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
 785 790 795 800
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
 805 810 815
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
 820 825 830
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
 835 840 845
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
 865 870 875 880
 Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
 885 890 895
 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990

Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005
 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
 1010 1015 1020
 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
 1025 1030 1035 1040
 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
 1045 1050 1055
 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
 1060 1065 1070
 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
 1075 1080 1085
 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
 1090 1095 1100
 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro
 1105 1110 1115 1120
 Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser
 1125 1130 1135
 Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu
 1140 1145 1150
 Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu
 1155 1160 1165
 Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
 1170 1175 1180
 Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met
 1185 1190 1195 1200
 Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
 1205 1210 1215
 Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
 1220 1225 1230
 Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
 1235 1240 1245
 Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile
 1250 1255 1260
 Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
 1265 1270 1275 1280
 Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys
 1285 1290 1295
 Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
 1300 1305 1310
 Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr

1315	1320	1325
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr 1330	1335	1340
Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser 1345	1350	1355 1360
Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu 1365	1370	1375
Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val 1380	1385	1390
Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys 1395	1400	1405
Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His 1410	1415	1420
Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly 1425	1430	1435 1440
Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr 1445	1450	1455
Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr 1460	1465	1470
Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val 1475	1480	1485
Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys 1490	1495	1500
Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe 1505	1510	1515 1520
Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu 1525	1530	1535
Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala 1540	1545	1550
Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His 1555	1560	1565
Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe 1570	1575	1580
Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser 1585	1590	1595 1600
His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly 1605	1610	1615
Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe 1620	1625	1630
Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val 1635	1640	1645

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1650 1655 1660
 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1665 1670 1675 1680
 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
 1685 1690 1695
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760
 Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
 1765 1770 1775
 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840
 Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
 1875 1880 1885
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965

Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
 1970 1975 1980
 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
 1985 1990 1995 2000
 His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
 2005 2010 2015
 Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
 2020 2025 2030
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
 2035 2040 2045
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
 2050 2055 2060
 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
 2065 2070 2075 2080
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
 2085 2090 2095
 Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
 2100 2105 2110
 Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
 2115 2120 2125
 Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
 2130 2135 2140
 Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
 2145 2150 2155 2160
 Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser
 2165 2170 2175
 Ser Ala Glu Val
 2180

<210> 140
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 <212> DNA
 <213> Homo sapiens

<400> 140
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22

<210> 141
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 141
 acaggaacct gctgtacgtg tac

23

<210> 142
 <211> 19
 <212> DNA
 <213> Homo sapiens

 <400> 142
 gaccattag gaggtctac 19

 <210> 143
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 143
 tatgtctcag tcacctacct g 21

 <210> 144
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: ClS7 primer

 <400> 144
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 <210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC7gAS1
 antisense primer

 <400> 145
 tgtcatgtac tgcactcgca cagc 24

 <210> 146
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC7AS14
 antisense primer

 <400> 146
 tcgtggctgc acaggatgcg ggtg 24

 <210> 147
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HC4AS3'
 antisense primer

 <400> 147
 cgggatccat tgtcacgta catctgc 27

 <210> 148
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC1AS3'Kpn
 antisense primer

 <400> 148
 cttggtacca cttcagcact agatgagatg 30

 <210> 149
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC2RACE1
 primer

 <400> 149
 aagagcagca tctcccgtaa acagtc 26

 <210> 150
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC2RACE2
 Primer

 <400> 150
 taacaagctc tgtgcttcct cttccg 26

 <210> 151
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: HC2RACE3
 PRIMER

 <400> 151
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Primer

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